

## **SUPPLEMENTARY MATERIALS**

### **Blood DNA methylation and breast cancer: A prospective case-cohort analysis in the Sister Study**

#### **Supplementary Methods**

##### **DNA extraction**

Genomic DNA was extracted from aliquots of whole blood using an automated system (Autopure LS, Gentra Systems) in the NIEHS Molecular Genetics Core Facility or using DNAQuik at BioServe Biotechnologies LTD (Beltsville, MD). One microgram of DNA from each woman was bisulfite-converted in 96-well plates using the EZ DNA Methylation Kit (Zymo Research, Orange County CA) and methylation analysis was carried out at the NIH Center for Inherited Disease Research at Johns Hopkins University (Baltimore, MD). Samples were tested for completion of bisulfite conversion, and converted DNA was analyzed on Illumina Human450 Methylation Arrays following the manufacturer's protocol. The arrays were analyzed with high throughput robotics to minimize batch effects.

##### **DNA methylation data preprocessing**

Methylation data preprocessing and quality control was completed using the *ENmix* R software package (1). This included the following steps: reducing background noise with ENmix method (1); correcting fluorescent dye-bias using RELIC method (2); quantile normalization to make

overall array fluorescence intensity distribution comparable between arrays and reducing Infinium I and II probe design bias using RCP method (3). A total of 62,012 CpG probes were excluded: 16,100 CpG probes with > 5% low quality data; 44,938 probes annotated as having 1) common SNPs (MAF>0.05 in HapMap CEU dataset) within 2 base pairs of probe target region, or 2) non-specific CpGs mapping to multiple genomic locations(4), or 3) on Y chromosome; and 974 CpGs with multi-modal distributions as determined with the *nmode* function in the ENmix R package.

We excluded 102 samples due to data quality issues: 91 samples that had average bisulfite intensity < 4000 or had more than 5% of probes with low-quality methylation values (detection p >0.000001, number of beads <3, or values outside of 3IQR); 4 samples that were outliers for their methylation beta value distributions; 1 sample with missing phenotype data; and 6 women whose date of diagnosis preceded blood draw. Methylation data preprocessing and quality control was completed using the ENmix R software package (1), including the following steps: ENmix background correction (1), RELIC dye bias correction (2), quantile normalization and RCP (3) probe design bias adjustment.

## Statistical analysis

Methylation was estimated using  $\beta$ -values calculated from fluorescence intensities for unmethylated (U) and methylated (M) alleles where  $\beta = M/(M+U+100)$ , with resulting  $\beta$ -values ranging from 0 (completely unmethylated) to 1 (100% methylated) (5). M-values (the logit transformation of  $\beta$ ) were used in all statistical tests. The association between breast cancer status and DNA methylation (M-value) for each CpG site was tested in Sister Study data using a case-cohort proportional hazard model adjusted for cell type proportions, the top 6 surrogate

variables based on array control-probes, and experimental plate (94 samples per plate). Age was treated as the primary time factor, with age at blood draw as the left truncation time and right censoring at age on September 2015. White blood cell type proportions were estimated with the Houseman method (6) using the R estimateCellCounts function in the minfi R package. To adjust for laboratory technical variation, the singular value decomposition (SVD) method was used on the set of non-negative array control-probes to estimate surrogate variables. The top 6 of these surrogate variables, accounting for 95% of array control-probe variation, were used for adjustment in association analyses. Association between breast cancer status and DNA methylation in EPIC-Italy dataset was tested using logistic regression with adjustment for age (in years). Association between time to diagnosis and DNA methylation level in Sister Study cases was evaluated using robust linear regression, adjusting for age, cell type proportions, the top 6 surrogate variables, and experiment plate variable.

### **Genetic association analysis**

We use the concept of Mendelian randomization to investigate potential causal relationships between DNA methylation and breast cancer. We used previously published Sister Study genotype data generated using the Illumina Infinium OncoArray 500K BeadChip (7). The OncoArray comprises approximately 500K SNPs, including a genome-wide backbone of 230K tag SNPs and additional SNPs covering cancer susceptibility, metabolism, and other endpoints (8). Similar to the method described in detail by Wahl et al(9) we carried out “causal analysis:” For each CpG that was associated with breast cancer, we performed linear regression to evaluate the association between CpG methylation and SNPs within 1Mb (excluding SNPs in probe regions). The SNP with strongest association P value with a CpG was designated as the “*cis*-

SNP”. For those *cis*-SNPs with statistically significant associations at a Bonferroni threshold, we then performed pairwise association analyses using linear regression to estimate coefficients  $\beta_{\text{CpG-SNP}}$ ,  $\beta_{\text{BCa-CpG}}$ , and  $\beta_{\text{BCa-SNP}}$ . Under a causality assumption, a *cis*-SNP affects breast cancer only through CpG methylation, so the predicted effect can be estimated as  $\beta_{\text{pred}} = \beta_{\text{CpG-SNP}} \times \beta_{\text{BCa-CpG}}$ . We then compared the correlation between predicted effects  $\beta_{\text{pred}}$  and observed effects  $\beta_{\text{BCa-SNP}}$ .

Again similar to the method described in detail by Wahl et al(9) we carried out “consequential analysis” to test whether DNA methylation is a consequence of breast cancer. Genetic risk scores (GRS) based on 313 previously-reported breast cancer susceptibility SNPs were calculated for each Sister Study participant as previously described (10). We then performed pairwise linear regression analysis to estimate coefficients  $\beta_{\text{BCa-GRS}}$ ,  $\beta_{\text{CpG-BCa}}$ , and  $\beta_{\text{CpG-GRS}}$ . Finally, we calculated the predicted effect of GRS on CpG methylation as  $\beta_{\text{pred}} = \beta_{\text{BCa-GRS}} \times \beta_{\text{CpG-BCa}}$ . and examined the correlation between observed and predicted effects.

## Pathway analysis

Based on genome build version GRCh37 gene annotation, we mapped each CpG on the Illumina 450K array to within 5kb of a unique gene. We then performed gene pathway analysis to investigate whether the canonical pathways in the Ingenuity Pathway Analysis (IPA) database (QIAGEN Inc.) were enriched with genes located around CpGs differentially methylated between breast cancer cases and controls. We calculated permutation P values using the results of 10000 random shuffles of association P values for the CpGs on the 450K array.

## Functional annotation

DNA methylation and histone modifications are both involved in gene regulation, and related pathways are often dependent on each other (11). To examine this in relationship to breast cancer, we mapped the 450K CpGs in relation to various histone marks generated from ENCODE Chip-Seq data for lymphoblasts and other cell types (12). We then tested whether histone peaks were enriched with CpGs differentially methylated between breast cancer cases and controls.

### References:

1. Xu Z, Niu L, Li L, *et al*. ENmix: a novel background correction method for Illumina HumanMethylation450 BeadChip. *Nucleic Acids Res* 2016;44(3):e20.
2. Xu Z, Langie SA, De Boever P, *et al*. RELIC: a novel dye-bias correction method for Illumina Methylation BeadChip. *BMC Genomics* 2017;18(1):4.
3. Niu L, Xu Z, Taylor JA. RCP: a novel probe design bias correction method for Illumina Methylation BeadChip. *Bioinformatics* 2016;32(17):2659-63.
4. Price ME, Cotton AM, Lam LL, *et al*. Additional annotation enhances potential for biologically-relevant analysis of the Illumina Infinium HumanMethylation450 BeadChip array. *Epigenetics Chromatin* 2013;6(1):4.
5. Bibikova M, Lin ZW, Zhou LX, *et al*. High-throughput DNA methylation profiling using universal bead arrays. *Genome Research* 2006;16(3):383-393.
6. Houseman EA, Accomando WP, Koestler DC, *et al*. DNA methylation arrays as surrogate measures of cell mixture distribution. *Bmc Bioinformatics* 2012;13.

7. Michailidou K, Lindstrom S, Dennis J, *et al.* Association analysis identifies 65 new breast cancer risk loci. *Nature* 2017;551(7678):92-94.
8. Amos CI, Dennis J, Wang Z, *et al.* The OncoArray Consortium: A Network for Understanding the Genetic Architecture of Common Cancers. *Cancer Epidemiol Biomarkers Prev* 2017;26(1):126-135.
9. Wahl S, Drong A, Lehne B, *et al.* Epigenome-wide association study of body mass index, and the adverse outcomes of adiposity. *Nature* 2017;541(7635):81-+.
10. Mavaddat N, Michailidou K, Dennis J, *et al.* Polygenic Risk Scores for Prediction of Breast Cancer and Breast Cancer Subtypes. *Am J Hum Genet* 2019;104(1):21-34.
11. Cedar H, Bergman Y. Linking DNA methylation and histone modification: patterns and paradigms. *Nat Rev Genet* 2009;10(5):295-304.
12. Consortium EP. An integrated encyclopedia of DNA elements in the human genome. *Nature* 2012;489(7414):57-74.

**Supplementary Table 1.** Differentially methylated CpGs (dmCpGs) between breast cancer invasive cases and non-cases\*

CpG	chr.	position	gene	coef_SS	p_SS	q_SS	coef_EPIC	z_EPIC	q_EPIC	coef_t2d	q_t2d
cg04902899	1	1717822	GNB1	-1.94	1.3E-08	1.5E-05	-0.94	-1.17	2.3E-01	0.01	2.5E-03
cg09255966	1	2334136	RER1	1.30	8.2E-10	2.1E-06	1.09	2.50	3.1E-02	0.01	2.2E-01
cg12578250	1	3343557	PRDM16	-1.44	2.8E-08	2.5E-05	-1.70	-2.81	1.6E-02	0.01	5.6E-02
ch.1.385573R	1	10464086	PGD	0.97	4.2E-08	3.2E-05	NA	NA	NA	-0.01	5.8E-02
cg23231974	1	11994899	PLOD1	2.30	8.1E-08	4.9E-05	0.50	0.56	3.8E-01	0.00	4.1E-01
cg25282951	1	15095376	KAZN	-1.13	5.1E-08	3.6E-05	-0.31	-0.95	2.8E-01	0.01	3.0E-02
ch.1.543953R	1	15965817	DDI2	1.46	1.4E-08	1.5E-05	1.60	3.36	4.4E-03	-0.01	5.8E-03
cg03429968	1	29245850	EPB41	-1.74	6.5E-10	1.8E-06	NA	NA	NA	0.01	8.1E-02
cg03976754	1	33330006	FNDC5	-1.37	8.0E-09	1.1E-05	-2.69	-4.70	1.0E-04	0.01	7.6E-03
cg11416597	1	33722623	ZNF362	-1.27	7.3E-09	1.0E-05	0.91	1.69	1.2E-01	0.00	5.4E-01
cg12212217	1	35916872	KIAA0319L	1.24	1.3E-08	1.4E-05	0.26	0.50	4.0E-01	-0.01	1.3E-04
cg17492152	1	39461048	AKIRIN1	-1.15	1.4E-08	1.5E-05	-1.25	-3.50	3.1E-03	0.01	5.3E-03
cg00162673	1	51700514	RNF11	-1.23	5.3E-13	1.5E-08	-2.25	-4.65	1.2E-04	0.01	5.2E-03
cg06826908	1	52155720	OSBPL9	-1.57	3.7E-09	6.4E-06	-1.20	-2.01	7.4E-02	0.01	7.7E-04
cg03935117	1	53191150	ZYG11B	1.50	4.7E-08	3.4E-05	0.34	0.49	4.0E-01	0.00	4.9E-01
cg26883190	1	53914086	NA	-1.97	2.9E-10	1.1E-06	-1.61	-3.74	1.6E-03	0.01	9.4E-03
cg22029640	1	55501145	PCSK9	-1.19	3.6E-08	2.9E-05	-0.77	-1.98	7.9E-02	0.01	2.9E-04
cg14709234	1	55684020	LOC100507634	-0.97	3.3E-08	2.8E-05	-1.59	-3.23	6.1E-03	0.01	1.3E-01
cg04486648	1	63190136	NA	2.02	3.3E-10	1.1E-06	0.83	1.38	1.8E-01	0.00	1.6E-01
cg11750112	1	64938742	CACHD1	-1.66	8.2E-08	4.9E-05	-2.57	-4.65	1.2E-04	0.01	1.2E-07
cg25344239	1	68326786	GNG12-AS1	1.70	7.0E-09	9.6E-06	-1.87	-2.96	1.2E-02	0.00	5.6E-01
cg02083528	1	78280850	FAM73A	-1.44	1.6E-09	3.5E-06	-1.80	-4.79	7.9E-05	0.01	1.5E-03
cg16678153	1	82265969	LPHN2	-0.81	6.0E-08	4.0E-05	1.63	3.18	6.8E-03	0.01	5.3E-03
cg09664975	1	84543551	PRKACB	-0.83	3.5E-09	6.1E-06	-2.07	-4.23	4.1E-04	0.02	2.7E-06
cg23253460	1	84709527	NA	-1.32	9.0E-09	1.2E-05	-2.01	-4.25	3.8E-04	0.00	2.7E-01
cg05393424	1	91403111	ZNF644	1.26	5.8E-09	8.5E-06	-0.94	-1.43	1.7E-01	-0.01	6.7E-03
cg21584883	1	93645960	TMED5	-0.82	1.3E-08	1.5E-05	-1.77	-3.87	1.1E-03	0.02	4.0E-05
cg27229407	1	103572615	COL11A1	-1.04	6.6E-09	9.4E-06	-0.04	-0.07	5.0E-01	0.01	1.6E-02
cg07470367	1	107684425	NTNG1	-1.02	1.0E-08	1.3E-05	-0.39	-0.83	3.1E-01	0.01	5.7E-02
cg09136695	1	111722281	CEPT1	-1.53	1.1E-09	2.6E-06	-1.37	-3.56	2.6E-03	0.01	3.2E-03
cg04126335	1	145525223	ITGA10	-1.07	1.4E-09	3.2E-06	-1.95	-2.25	5.0E-02	-0.01	5.6E-02
cg26884161	1	151303917	PI4KB	-1.52	8.2E-15	1.2E-09	-1.21	-3.29	5.2E-03	0.01	4.3E-02
cg06698332	1	151967449	S100A10	-1.58	5.9E-10	1.7E-06	-1.93	-4.28	3.5E-04	0.01	2.1E-03
cg16008440	1	161983790	OLFML2B	-1.49	1.1E-09	2.7E-06	-1.16	-3.58	2.5E-03	0.01	5.4E-05
cg00152047	1	166893354	ILDR2	1.31	1.4E-08	1.5E-05	-0.09	-0.15	4.8E-01	-0.01	1.4E-02

cg12427162	1	168198488	SFT2D2	-0.96	4.7E-08	3.4E-05	-0.80	-2.27	4.8E-02	0.00	4.7E-01
cg19723678	1	178241791	RASAL2	-1.41	1.3E-08	1.5E-05	-1.23	-2.26	4.9E-02	0.01	1.4E-05
cg00158654	1	192285333	RGS21	0.77	1.7E-08	1.7E-05	-1.17	-1.90	8.9E-02	-0.04	7.9E-15
cg23627149	1	193155273	B3GALT2	1.18	4.2E-12	6.3E-08	-1.96	-2.58	2.6E-02	-0.04	7.6E-18
cg25768273	1	211911579	NA	-1.16	4.5E-08	3.4E-05	-1.41	-4.95	5.2E-05	0.01	1.1E-03
cg07031542	1	214567074	PTPN14	-1.29	2.6E-09	5.1E-06	-2.20	-5.15	3.1E-05	0.01	4.6E-05
cg13865248	1	214842875	NA	-1.35	1.2E-08	1.4E-05	-1.46	-3.77	1.5E-03	0.01	3.2E-03
cg14468913	1	218338809	NA	-0.79	9.4E-08	5.3E-05	0.61	1.28	2.0E-01	0.03	2.7E-11
cg11976166	1	218520090	LOC728463	-1.49	1.6E-11	1.2E-07	0.67	1.35	1.9E-01	0.00	4.9E-01
cg14253939	1	228674594	RNF187	2.02	1.5E-08	1.6E-05	-0.45	-0.74	3.4E-01	-0.01	7.5E-03
cg20234959	1	236237760	NA	-1.55	3.6E-08	2.9E-05	-2.05	-3.07	9.1E-03	0.01	3.7E-04
cg17895289	1	241682884	FH	-1.72	1.2E-09	2.9E-06	-2.56	-2.92	1.3E-02	0.01	3.2E-09
cg22637834	1	244007281	AKT3	1.08	2.4E-09	4.7E-06	-0.32	-0.34	4.4E-01	-0.04	5.6E-22
cg19503731	1	244007303	AKT3	0.94	3.4E-09	6.0E-06	0.78	0.96	2.8E-01	-0.04	9.6E-18
cg03990819	2	434332	NA	1.26	2.9E-08	2.5E-05	0.49	0.96	2.8E-01	0.00	6.1E-01
cg17918270	2	1983484	MYT1L	-1.78	6.2E-12	7.3E-08	-0.81	-1.50	1.6E-01	0.00	6.3E-01
cg05977776	2	3741732	ALLC	1.46	9.5E-08	5.3E-05	0.39	0.85	3.1E-01	0.00	6.5E-01
cg26569634	2	10760591	NOL10	-1.14	5.0E-09	7.9E-06	-1.37	-4.20	4.4E-04	0.01	9.1E-04
cg13769605	2	12857067	TRIB2	-1.19	1.4E-08	1.5E-05	-1.60	-2.77	1.8E-02	0.01	9.9E-02
cg17940200	2	19170947	NA	1.48	8.6E-08	5.0E-05	-2.09	-2.57	2.7E-02	-0.01	2.3E-06
cg04819081	2	24026544	ATAD2B	0.81	1.3E-09	3.2E-06	-1.90	-3.61	2.3E-03	-0.05	4.2E-18
cg00008800	2	38710171	NA	-0.94	1.8E-10	7.8E-07	-2.65	-4.67	1.1E-04	-0.01	1.1E-01
cg03754165	2	60780427	BCL11A	0.83	2.0E-08	2.0E-05	1.96	4.15	5.0E-04	-0.02	1.2E-05
cg22727572	2	63272334	LOC100132215	1.64	2.6E-08	2.3E-05	-5.87	-5.20	2.8E-05	-0.02	4.4E-15
cg24726965	2	63606136	WDPCP	0.81	1.3E-11	1.1E-07	-1.40	-2.51	3.1E-02	-0.05	4.9E-19
cg16976189	2	67624291	ETAA1	-1.16	1.9E-10	8.0E-07	1.79	3.11	8.3E-03	0.02	2.8E-10
cg26364903	2	67624840	ETAA1	-0.72	2.6E-08	2.3E-05	-1.60	-2.83	1.6E-02	0.03	4.8E-08
cg07591442	2	69615105	GFPT1	-1.92	8.2E-08	4.9E-05	-0.55	-0.68	3.5E-01	0.01	1.4E-02
cg18850112	2	70329648	NA	-0.95	8.7E-09	1.2E-05	-1.06	-3.61	2.3E-03	0.01	3.5E-01
cg23400904	2	70418872	C2orf42	-1.77	5.5E-08	3.8E-05	-1.17	-1.67	1.2E-01	0.01	3.1E-03
cg24690060	2	77329502	LRRTM4	1.12	9.3E-09	1.2E-05	-2.02	-3.89	1.1E-03	-0.02	5.6E-05
cg18611949	2	86668510	KDM3A	-1.22	4.8E-09	7.8E-06	-1.10	-1.95	8.2E-02	0.02	1.7E-07
cg03037033	2	86668736	KDM3A	-1.95	8.4E-08	4.9E-05	0.75	0.85	3.1E-01	0.01	6.5E-05
cg05999729	2	98369433	NA	-1.26	2.3E-09	4.7E-06	-1.44	-4.32	3.1E-04	0.01	4.9E-02
cg24654185	2	99812274	MRPL30	-0.94	3.0E-08	2.6E-05	-1.17	-3.71	1.7E-03	0.01	9.0E-02
cg22865501	2	105321544	NA	-2.27	2.6E-09	5.0E-06	-0.91	-1.42	1.7E-01	0.01	9.6E-04
cg23562675	2	120107745	C2orf76	-1.30	2.9E-10	1.1E-06	-1.43	-4.32	3.1E-04	0.01	2.8E-03
cg27418500	2	123758682	NA	1.57	1.1E-08	1.4E-05	-1.28	-1.84	9.8E-02	-0.01	1.1E-02
cg18991132	2	128475701	WDR33	-1.77	8.0E-09	1.1E-05	-0.92	-1.33	1.9E-01	0.01	3.2E-07
cg01580574	2	134949671	NA	-0.99	1.6E-09	3.5E-06	-0.89	-3.42	3.8E-03	0.01	2.6E-01
cg04330811	2	134949779	NA	-2.10	6.5E-11	3.7E-07	-1.17	-1.98	7.9E-02	0.01	7.2E-05

cg12968518	2	148602504	ACVR2A	-0.51	7.6E-08	4.7E-05	2.01	4.82	7.4E-05	0.02	3.6E-02
cg02095456	2	153189667	FMNL2	-1.46	5.1E-08	3.6E-05	-1.57	-2.82	1.6E-02	0.01	1.2E-05
cg26480091	2	156403454	NA	0.95	5.0E-09	7.9E-06	-1.47	-2.10	6.5E-02	-0.03	4.2E-10
cg00322319	2	162094696	NA	-1.09	1.9E-08	1.8E-05	1.43	2.35	4.1E-02	0.02	9.6E-08
cg12649175	2	162927003	DPP4	1.83	5.7E-11	3.3E-07	1.40	2.49	3.2E-02	-0.01	4.3E-05
cg23138119	2	163218380	GCA	0.68	4.8E-09	7.8E-06	-2.60	-3.06	9.3E-03	-0.06	1.5E-20
cg08943393	2	166325622	CSRNP3	1.13	1.6E-08	1.6E-05	-2.18	-3.01	1.0E-02	-0.02	1.3E-11
cg06371280	2	172017419	TLK1	-1.61	1.4E-11	1.2E-07	-0.86	-1.36	1.9E-01	0.01	1.9E-02
cg12191300	2	174873689	NA	-1.34	7.9E-08	4.8E-05	-0.73	-1.46	1.6E-01	0.00	4.9E-01
cg14528756	2	176862893	KIAA1715	1.04	1.1E-09	2.6E-06	-0.18	-0.24	4.6E-01	-0.03	8.1E-12
cg10671757	2	180722610	MIR1258	1.22	6.1E-08	4.0E-05	0.60	1.62	1.3E-01	0.00	3.1E-01
cg25783997	2	185462928	ZNF804A	-0.75	2.9E-08	2.5E-05	-2.00	-4.81	7.4E-05	0.02	3.7E-03
cg22374415	2	188210673	CALCRL	0.85	9.4E-09	1.2E-05	-1.58	-2.72	2.0E-02	-0.04	9.2E-17
cg25202000	2	188754840	NA	0.97	9.0E-08	5.2E-05	-1.25	-1.91	8.8E-02	-0.02	6.0E-08
cg23466916	2	192543328	NABP1	-1.23	9.3E-09	1.2E-05	-0.42	-0.67	3.6E-01	0.01	5.6E-03
cg26510700	2	193467276	NA	1.33	6.7E-09	9.5E-06	1.51	2.00	7.6E-02	-0.01	2.7E-05
cg05059169	2	198339611	COQ10B	-1.81	1.2E-08	1.4E-05	-2.40	-3.46	3.4E-03	0.01	3.5E-03
cg08172999	2	200775722	C2orf69	-0.95	3.6E-08	2.9E-05	1.94	4.43	2.3E-04	0.02	6.6E-06
cg22902939	2	201355148	KCTD18	2.85	2.0E-08	1.9E-05	5.49	3.64	2.1E-03	0.00	7.4E-03
cg23281307	2	202142817	CASP8	-1.56	6.4E-08	4.2E-05	0.02	0.04	5.0E-01	0.01	3.6E-02
cg03555299	2	206830681	NA	-1.85	4.2E-10	1.3E-06	-1.59	-3.35	4.5E-03	0.01	1.5E-02
cg25300234	2	212938740	ERBB4	1.04	1.7E-08	1.7E-05	-1.17	-1.72	1.2E-01	-0.02	5.9E-09
cg00011346	2	213403859	ERBB4	-0.89	3.2E-08	2.7E-05	0.07	0.22	4.6E-01	0.01	3.0E-01
cg02540338	2	217243695	NA	-1.44	2.0E-08	1.9E-05	-1.19	-3.39	4.1E-03	0.01	2.5E-03
cg09151613	2	218301065	DIRC3	1.49	8.3E-08	4.9E-05	-0.13	-0.31	4.4E-01	-0.01	1.0E-01
cg12267933	2	228176991	LOC654841	-1.23	1.6E-08	1.7E-05	-1.15	-2.96	1.2E-02	0.01	1.6E-01
cg06193628	2	228526145	NA	1.38	9.5E-08	5.3E-05	0.35	0.61	3.7E-01	0.00	4.4E-01
cg25995995	2	240927173	NDUFA10	-2.07	4.4E-09	7.4E-06	-3.13	-3.65	2.1E-03	0.01	1.2E-02
cg27502952	2	242351401	FARP2	-1.35	2.8E-08	2.5E-05	-0.49	-1.17	2.3E-01	0.01	3.8E-02
cg05643613	3	11592649	ATG7	-1.77	6.9E-09	9.5E-06	-1.67	-2.15	6.0E-02	0.01	7.8E-06
cg05575304	3	11607115	VGLL4	-1.28	3.1E-08	2.6E-05	-0.72	-1.40	1.8E-01	0.00	2.2E-01
cg21331107	3	32541698	CMTM6	-1.38	2.0E-08	1.9E-05	-2.21	-4.11	5.7E-04	0.00	3.2E-01
ch.3.1113149F	3	51461419	VPRBP	1.13	3.5E-08	2.8E-05	1.20	2.20	5.4E-02	0.00	4.0E-01
cg04104820	3	52291169	WDR82	-1.09	1.9E-09	4.1E-06	3.44	5.11	3.4E-05	0.02	5.3E-12
cg04606669	3	52318566	GLYCTK	-1.40	4.9E-08	3.5E-05	-1.74	-3.13	7.8E-03	0.01	3.4E-05
cg24980696	3	56720960	FAM208A	-1.62	4.4E-08	3.3E-05	-0.55	-0.90	2.9E-01	0.00	4.5E-01
cg15023858	3	69812434	MITF	-1.55	4.0E-08	3.1E-05	-1.69	-2.65	2.3E-02	0.01	4.8E-03
cg15963983	3	71020458	FOXP1	-1.66	5.9E-08	3.9E-05	-0.91	-1.61	1.4E-01	0.01	5.4E-04
cg01551787	3	72982378	GXYLT2	-1.34	6.5E-08	4.2E-05	-1.47	-3.37	4.3E-03	0.01	2.7E-02
cg04326887	3	73086974	PPP4R2	-1.66	6.5E-08	4.2E-05	-0.81	-1.34	1.9E-01	0.00	1.6E-01
cg19385799	3	78164711	NA	-1.99	1.2E-12	2.2E-08	-1.80	-4.21	4.3E-04	0.02	5.4E-07

cg11630696	3	79817333	ROBO1	-0.71	9.3E-08	5.3E-05	2.40	4.47	2.0E-04	0.03	1.0E-07
cg03202213	3	85006115	CADM2	1.15	6.1E-08	4.0E-05	-1.65	-2.40	3.7E-02	-0.02	5.4E-08
cg06006512	3	89221147	EPHA3	0.90	4.3E-08	3.3E-05	-0.40	-0.61	3.7E-01	-0.02	4.4E-08
cg01954930	3	94656939	LINC00879	1.77	1.2E-08	1.4E-05	-4.17	-3.73	1.6E-03	-0.01	4.5E-11
cg12927270	3	94656950	LINC00879	1.59	1.9E-08	1.9E-05	-2.49	-2.23	5.1E-02	-0.01	3.8E-09
cg14959291	3	96532006	EPHA6	-0.81	3.2E-10	1.1E-06	-0.19	-0.46	4.1E-01	0.04	2.4E-13
cg15093079	3	96533290	EPHA6	-1.19	4.4E-08	3.3E-05	1.88	2.56	2.7E-02	0.02	1.4E-07
cg25160554	3	97483242	ARL6	-1.29	1.5E-09	3.3E-06	-0.36	-0.68	3.5E-01	0.02	1.9E-07
cg08470013	3	97805957	OR5AC2	1.15	4.2E-11	2.6E-07	-0.81	-1.33	1.9E-01	-0.03	1.8E-12
cg24685239	3	105159482	ALCAM	1.39	7.6E-08	4.7E-05	-0.94	-1.31	2.0E-01	-0.01	1.2E-03
cg24124753	3	120461562	GTF2E1	1.95	2.2E-08	2.0E-05	1.80	2.20	5.5E-02	0.00	7.9E-02
cg16588007	3	123300842	PTPLB	-1.58	5.1E-09	7.9E-06	-0.70	-1.17	2.3E-01	0.01	1.9E-02
cg04872851	3	127007606	NA	1.01	7.5E-08	4.7E-05	-2.27	-4.14	5.2E-04	-0.01	6.6E-04
cg00911289	3	128840257	RAB43	-1.24	4.7E-08	3.4E-05	-1.19	-1.95	8.2E-02	0.01	2.0E-01
cg07038342	3	145969625	PLSCR4	1.12	4.2E-08	3.2E-05	0.12	0.16	4.8E-01	-0.02	1.2E-04
cg10723575	3	149422266	WWTR1	-2.15	6.4E-12	7.3E-08	-2.44	-4.11	5.8E-04	0.01	1.5E-04
cg26690511	3	155422103	PLCH1	-0.93	2.9E-09	5.5E-06	-0.59	-1.86	9.5E-02	0.00	5.4E-01
cg24837026	3	155607265	GMPS	-1.43	8.1E-12	8.3E-08	-1.61	-3.26	5.7E-03	0.01	3.3E-04
cg14995416	3	159713351	IL12A	-1.26	4.0E-08	3.1E-05	-1.63	-3.63	2.2E-03	0.00	3.3E-01
cg25699837	3	163722294	NA	0.97	2.3E-08	2.2E-05	0.23	0.36	4.3E-01	-0.02	2.0E-10
cg23535170	3	179489892	USP13	-0.95	3.8E-08	3.0E-05	-1.41	-4.81	7.6E-05	0.01	2.8E-02
cg12196367	3	183892577	AP2M1	1.79	7.3E-08	4.6E-05	1.60	1.88	9.1E-02	0.00	4.4E-01
cg24007445	3	194224524	NA	-1.44	6.4E-08	4.2E-05	-1.21	-2.34	4.3E-02	0.00	4.1E-01
cg11116094	4	3278748	NA	-1.67	9.0E-09	1.2E-05	0.54	0.74	3.3E-01	0.00	6.9E-01
cg25889581	4	16708336	LDB2	1.35	2.9E-09	5.5E-06	0.69	1.61	1.4E-01	-0.01	2.0E-01
cg04177287	4	21857313	KCNIP4-IT1	1.13	5.2E-08	3.7E-05	0.12	0.33	4.4E-01	0.00	3.4E-01
cg14837557	4	25158468	SEPSECS	1.16	5.2E-09	8.0E-06	-0.88	-1.88	9.2E-02	-0.01	3.7E-04
cg25289973	4	41362397	LIMCH1	-1.55	6.5E-08	4.2E-05	-0.58	-1.51	1.5E-01	0.00	7.2E-01
cg09491068	4	41478990	LIMCH1	1.99	1.1E-08	1.3E-05	1.49	2.23	5.2E-02	0.00	7.0E-01
cg16511076	4	48887480	OClAD2	-1.46	4.6E-08	3.4E-05	-1.29	-2.40	3.8E-02	0.01	4.7E-02
cg24140037	4	56499522	NMU	1.65	5.8E-09	8.5E-06	-0.05	-0.07	5.0E-01	-0.01	4.9E-04
cg26737330	4	71200323	CABS1	-1.16	2.7E-09	5.1E-06	-1.35	-3.22	6.3E-03	0.01	1.2E-01
cg03578005	4	77170672	FAM47E-STBD1	-1.51	1.0E-08	1.3E-05	-1.65	-2.91	1.3E-02	0.00	5.1E-01
cg23629643	4	77547320	SHROOM3	-1.45	1.2E-08	1.4E-05	-0.56	-1.07	2.5E-01	0.01	6.4E-03
cg25710815	4	89300116	HERC6	-1.15	1.8E-08	1.8E-05	3.61	3.94	9.2E-04	0.02	8.8E-09
cg25617092	4	93225157	GRID2	-1.43	2.2E-09	4.5E-06	0.10	0.19	4.7E-01	0.01	1.5E-02
cg25433855	4	102268622	PPP3CA	-1.01	4.1E-08	3.2E-05	-0.60	-1.09	2.5E-01	0.01	4.5E-03
cg06501333	4	103419193	NFKB1	1.13	1.0E-09	2.5E-06	-2.24	-4.37	2.7E-04	-0.02	4.3E-08
cg15508749	4	109115092	NA	-1.40	3.9E-09	6.5E-06	-0.66	-1.37	1.8E-01	0.00	6.5E-01
cg02945007	4	141294667	SCOC	-1.20	6.5E-08	4.2E-05	-1.14	-2.01	7.5E-02	0.01	2.0E-01
cg13848802	4	144434253	SMARCA5	-0.90	6.8E-08	4.4E-05	0.17	0.38	4.3E-01	0.01	3.8E-02

cg13945578	4	164265822	NPY5R	-1.16	8.3E-12	8.3E-08	-0.41	-0.83	3.1E-01	0.02	5.9E-09
cg12267786	4	164395093	TKTL2	1.85	1.8E-08	1.8E-05	1.26	1.59	1.4E-01	-0.01	4.2E-09
cg05982597	4	177654753	VEGFC	0.88	7.9E-11	4.1E-07	-2.22	-3.33	4.7E-03	-0.04	4.2E-18
ch.4.3383604F	4	184607857	TRAPPC11	-0.85	5.0E-09	7.9E-06	0.78	1.86	9.5E-02	0.04	2.6E-16
cg26992150	4	184917686	STOX2	-1.15	8.1E-08	4.9E-05	-1.31	-2.81	1.6E-02	0.01	1.4E-01
cg09547427	5	1055427	SLC12A7	-1.56	9.6E-09	1.2E-05	-1.48	-2.17	5.8E-02	0.01	8.6E-03
cg05660889	5	6687293	LOC100505625	-0.96	9.5E-08	5.3E-05	1.05	1.94	8.4E-02	0.01	2.0E-04
cg02452058	5	9430822	SEMA5A	1.46	4.0E-08	3.1E-05	-1.18	-2.12	6.3E-02	-0.01	1.1E-03
cg01021224	5	35049428	AGXT2	-1.45	1.5E-09	3.4E-06	-1.21	-4.16	5.0E-04	0.01	2.5E-02
cg07316489	5	36876114	LOC646719	-1.07	6.5E-09	9.2E-06	0.12	0.24	4.6E-01	0.01	7.1E-04
cg26077283	5	37815776	GDNF	1.54	1.0E-08	1.3E-05	-1.84	-3.05	9.4E-03	0.00	3.3E-01
cg01691522	5	42998521	NA	-1.57	1.3E-08	1.5E-05	-0.84	-1.26	2.1E-01	0.00	4.0E-01
cg00955895	5	43190083	NIM1	-2.00	1.5E-11	1.2E-07	-0.58	-0.95	2.8E-01	0.01	2.0E-06
cg14703610	5	56206110	SETD9	-1.13	3.9E-08	3.0E-05	-1.49	-2.16	5.9E-02	0.01	4.0E-04
cg19977964	5	56206213	SETD9	-1.14	6.8E-09	9.5E-06	2.36	4.19	4.5E-04	0.01	3.6E-04
cg14051306	5	56248243	MIER3	-2.13	4.6E-09	7.5E-06	-1.29	-1.81	1.0E-01	0.00	6.1E-01
cg23123909	5	57878953	RAB3C	-1.49	1.7E-10	7.5E-07	-1.45	-3.17	7.1E-03	0.01	3.9E-03
cg08463715	5	60050299	ELOVL7	1.36	1.3E-08	1.4E-05	-0.75	-0.91	2.9E-01	-0.02	1.1E-08
cg07180460	5	60627633	ZSWIM6	-1.40	8.9E-08	5.1E-05	-0.20	-0.30	4.5E-01	0.00	2.5E-01
cg23961757	5	95122534	RHOBTB3	-1.51	6.8E-14	3.8E-09	-1.21	-3.31	5.0E-03	0.01	7.5E-04
cg00096106	5	100176809	ST8SIA4	-0.77	9.5E-09	1.2E-05	0.04	0.11	4.9E-01	0.02	4.2E-03
cg20402000	5	107007640	EFNA5	-1.30	1.5E-08	1.6E-05	0.40	0.68	3.5E-01	0.00	3.4E-01
cg01885839	5	111017556	STARD4-AS1	-2.36	3.1E-09	5.8E-06	-3.17	-4.34	3.0E-04	0.01	5.8E-04
cg18422875	5	113697897	KCNN2	-1.25	5.0E-09	7.9E-06	-0.19	-0.39	4.2E-01	0.00	7.2E-01
cg08870042	5	114938148	TICAM2	-1.02	8.4E-09	1.1E-05	-1.24	-2.61	2.5E-02	0.01	2.1E-01
cg24770230	5	115194332	AP3S1	-1.00	2.5E-08	2.3E-05	-1.08	-2.50	3.1E-02	0.01	1.6E-01
cg01214384	5	120179610	NA	1.46	2.4E-08	2.2E-05	0.66	1.70	1.2E-01	-0.01	1.0E-01
ch.5.2320326F	5	126871056	PRRC1	-0.78	7.9E-10	2.1E-06	1.45	3.16	7.3E-03	0.04	4.1E-13
cg01939274	5	127874478	FBN2	-1.44	3.4E-10	1.1E-06	1.81	2.69	2.1E-02	0.01	2.9E-05
cg10825350	5	132541078	FSTL4	-1.38	1.9E-11	1.4E-07	-1.21	-3.74	1.6E-03	0.01	4.9E-05
cg19780570	5	133764548	NA	-1.07	2.5E-08	2.3E-05	-1.74	-4.05	6.7E-04	0.01	4.4E-03
cg18019515	5	142783385	NR3C1	-1.52	8.2E-08	4.9E-05	-0.96	-0.87	3.0E-01	0.00	3.7E-01
cg21611262	5	145252443	GRXCR2	1.85	5.6E-08	3.8E-05	0.23	0.40	4.2E-01	-0.01	3.2E-02
ch.5.2738996F	5	145864698	TCERG1	-1.05	1.7E-11	1.3E-07	2.02	4.22	4.2E-04	0.03	1.2E-09
cg08418508	5	159830462	C5orf54	1.71	8.8E-08	5.1E-05	-1.29	-2.16	5.9E-02	-0.01	2.9E-02
cg13902409	5	179922147	CNOT6	-1.65	5.6E-09	8.4E-06	-1.61	-2.96	1.2E-02	0.01	1.3E-01
cg02456218	5	180476573	BTNL9	-1.07	8.9E-08	5.1E-05	-2.37	-4.31	3.2E-04	0.00	6.7E-01
cg18185178	6	1516613	NA	-2.55	6.8E-09	9.5E-06	-1.47	-1.83	9.9E-02	0.01	1.4E-04
cg04455567	6	3425259	SLC22A23	-1.45	2.4E-08	2.2E-05	-1.70	-2.82	1.6E-02	0.01	3.9E-02
cg23819836	6	15663134	DTNBP1	0.91	1.3E-08	1.5E-05	2.22	4.07	6.5E-04	0.00	7.0E-01
cg23902105	6	22009091	LINC00340	1.20	8.4E-08	4.9E-05	0.36	0.95	2.8E-01	0.00	5.5E-01

cg14840502	6	22623897	NA	1.13	6.7E-08	4.3E-05	-2.17	-3.59	2.4E-03	-0.02	2.5E-09
cg19082069	6	26018534	HIST1H1A	-2.38	2.3E-09	4.7E-06	-2.16	-3.76	1.5E-03	0.01	2.4E-07
cg21331362	6	26221330	HIST1H3E	-1.08	4.8E-08	3.5E-05	-1.08	-1.90	8.9E-02	0.00	7.1E-01
cg06079966	6	26237621	HIST1H1D	-1.59	7.6E-09	1.0E-05	-2.42	-4.50	1.9E-04	0.00	4.2E-01
cg09333077	6	27118882	MIR3143	-1.19	1.4E-08	1.5E-05	-0.80	-2.02	7.4E-02	0.01	1.0E-03
cg26526443	6	27141658	NA	-1.18	5.2E-10	1.6E-06	-1.53	-4.92	5.5E-05	0.01	1.6E-02
cg11052668	6	28626564	NA	1.54	2.4E-10	9.0E-07	1.67	3.23	6.1E-03	-0.01	2.1E-04
cg24152718	6	30185818	TRIM26	-1.96	2.0E-09	4.2E-06	-2.05	-3.92	9.8E-04	0.01	4.8E-07
cg11606826	6	30540994	ABCF1	1.68	8.4E-08	4.9E-05	-2.02	-2.74	1.9E-02	0.00	2.5E-01
cg24915236	6	31936514	STK19	-1.24	7.1E-08	4.5E-05	0.15	0.25	4.6E-01	0.01	3.3E-03
cg19494811	6	34356253	NUDT3	-1.54	2.0E-08	2.0E-05	-1.64	-3.70	1.8E-03	0.00	1.8E-01
cg18726036	6	35543610	FKBP5	-2.59	1.3E-10	6.1E-07	-3.63	-4.30	3.3E-04	0.01	2.3E-04
cg01980126	6	42835840	GLTSCR1L	-2.02	2.0E-11	1.5E-07	-1.45	-2.42	3.7E-02	0.01	3.5E-02
cg21911007	6	43549627	POLH	-1.05	8.9E-09	1.2E-05	-0.59	-1.53	1.5E-01	0.01	9.4E-02
cg14739378	6	46655306	TDRD6	2.11	8.4E-08	4.9E-05	-2.79	-2.14	6.0E-02	-0.01	2.3E-02
cg26714205	6	49522045	C6orf141	-1.11	1.0E-09	2.6E-06	-0.77	-2.83	1.6E-02	0.01	2.3E-02
cg01326123	6	63157784	NA	0.92	2.7E-08	2.4E-05	-0.74	-1.15	2.3E-01	-0.03	7.2E-15
cg16955101	6	64283916	PTP4A1	-1.19	3.1E-09	5.8E-06	0.02	0.03	5.1E-01	0.02	1.8E-07
cg23756322	6	72924771	RIMS1	0.75	3.6E-08	2.9E-05	-0.90	-1.85	9.6E-02	-0.03	2.0E-10
cg13921196	6	76603364	MYO6	-0.71	2.2E-10	8.5E-07	-0.17	-0.38	4.3E-01	0.05	1.3E-14
cg08287994	6	79788234	PHIP	-1.76	6.3E-10	1.8E-06	-2.28	-3.02	1.0E-02	0.02	2.4E-14
cg07493837	6	96025317	MANEA	-1.44	3.5E-10	1.1E-06	2.13	2.90	1.3E-02	0.01	1.2E-02
cg08747277	6	96048126	MANEA	0.97	1.6E-09	3.5E-06	-1.36	-1.87	9.3E-02	-0.04	2.8E-16
cg18709589	6	96969512	UFL1	-1.00	5.9E-09	8.7E-06	0.92	1.85	9.6E-02	0.02	2.7E-06
cg23429981	6	97345948	NDUFAF4	1.37	3.5E-11	2.4E-07	2.11	2.90	1.3E-02	-0.01	1.5E-02
cg07439409	6	97731296	MMS22L	0.97	9.2E-08	5.3E-05	2.29	4.37	2.7E-04	-0.01	1.2E-01
cg06539434	6	101120796	ASCC3	0.53	3.2E-09	5.8E-06	-1.66	-2.90	1.3E-02	-0.07	4.2E-18
cg05099288	6	109700555	CD164	1.02	6.4E-08	4.2E-05	1.87	3.97	8.4E-04	-0.01	2.8E-03
cg04443690	6	113370857	NA	1.25	1.3E-08	1.5E-05	-1.57	-2.79	1.7E-02	-0.01	6.0E-03
cg04008905	6	142644368	GPR126	1.17	4.8E-09	7.8E-06	-1.73	-2.91	1.3E-02	-0.02	2.0E-10
cg04409048	6	146203625	LOC100507557	1.60	4.8E-08	3.4E-05	-1.95	-2.78	1.7E-02	-0.01	1.0E-02
cg25157874	6	163835117	CAHM	-1.15	1.0E-10	5.0E-07	-0.09	-0.17	4.8E-01	0.02	3.0E-05
cg24310785	6	163985223	QKI	0.92	9.6E-08	5.4E-05	-2.40	-3.98	8.3E-04	-0.02	6.2E-07
cg08066917	6	167764146	NA	1.74	3.2E-09	5.8E-06	-1.73	-1.44	1.7E-01	-0.02	1.8E-21
cg22229470	6	168107104	NA	0.64	6.7E-08	4.3E-05	1.20	2.26	4.9E-02	-0.03	1.6E-07
cg13517866	6	168970787	SMOC2	-1.69	2.9E-08	2.5E-05	-1.30	-2.63	2.4E-02	0.01	7.8E-05
cg14671926	6	169930772	WDR27	-1.08	1.7E-08	1.7E-05	0.66	2.10	6.5E-02	0.02	7.1E-05
cg16840616	7	93831	NA	-2.60	6.7E-11	3.7E-07	1.40	2.07	6.8E-02	0.01	2.0E-06
cg18454990	7	1178137	C7orf50	-0.87	6.2E-08	4.1E-05	-1.22	-2.21	5.3E-02	0.02	1.2E-03
cg04849508	7	2801959	GNA12	-1.63	5.3E-08	3.7E-05	-0.44	-0.90	2.9E-01	0.01	7.6E-04
cg06914774	7	2908787	NA	-1.00	3.9E-08	3.1E-05	-0.86	-3.29	5.3E-03	0.01	1.0E-01

cg05460950	7	4800661	FOXK1	1.84	2.3E-12	3.9E-08	-1.24	-2.09	6.6E-02	0.00	4.8E-01
cg19934194	7	6286149	CYTH3	-1.42	4.4E-08	3.3E-05	-0.49	-0.63	3.7E-01	0.00	5.6E-01
cg02035961	7	6288071	CYTH3	1.30	2.8E-08	2.5E-05	0.18	0.33	4.4E-01	0.00	6.0E-01
cg17345859	7	6728525	ZNF12	-1.53	3.5E-08	2.8E-05	-2.07	-4.26	3.7E-04	0.01	2.0E-02
cg22850258	7	16438702	ISPD	-1.37	5.1E-10	1.6E-06	NA	NA	NA	0.01	1.4E-02
cg19057076	7	16438851	ISPD	-1.67	3.5E-13	1.1E-08	-0.59	-1.18	2.3E-01	0.01	2.4E-03
cg00755064	7	23749991	STK31	2.11	7.7E-09	1.0E-05	-3.83	-2.56	2.8E-02	-0.01	1.8E-13
cg03943571	7	24612635	MPP6	-1.29	1.2E-08	1.4E-05	1.87	2.52	3.0E-02	0.01	3.5E-02
cg20890313	7	26904699	SKAP2	-1.01	4.2E-08	3.2E-05	0.95	1.96	8.2E-02	0.01	2.6E-04
cg18243542	7	27843409	TAX1BP1	1.18	1.7E-08	1.7E-05	-1.57	-2.44	3.5E-02	-0.02	5.9E-13
cg08784317	7	39731097	RALA	-1.82	1.6E-08	1.7E-05	-0.89	-1.01	2.7E-01	0.00	2.0E-01
cg26203572	7	47797675	LINC00525	1.09	2.7E-33	7.6E-28	-3.94	-5.46	1.5E-05	0.02	2.3E-03
cg09921682	7	50133131	ZPBP	1.93	6.4E-08	4.2E-05	-4.44	-4.10	5.9E-04	-0.01	3.8E-03
cg00350885	7	50860872	GRB10	-1.16	8.1E-08	4.9E-05	-0.94	-1.79	1.1E-01	0.00	2.9E-01
cg18553202	7	63893881	LOC649395	0.92	5.3E-08	3.7E-05	-1.67	-2.37	4.0E-02	-0.03	3.0E-15
cg24495177	7	64362326	ZNF273	-1.01	4.6E-08	3.4E-05	-2.78	-4.18	4.7E-04	0.01	4.0E-02
cg04709675	7	75541952	POR	1.90	1.4E-08	1.5E-05	0.13	0.21	4.7E-01	0.00	6.3E-01
cg18092665	7	80732349	NA	0.99	3.0E-11	2.1E-07	-1.43	-2.32	4.4E-02	-0.03	9.1E-13
cg06405430	7	82446070	PCLO	0.78	1.2E-08	1.4E-05	-1.57	-2.86	1.5E-02	-0.03	1.1E-07
cg10412943	7	97739696	LMTK2	-1.30	1.1E-10	5.5E-07	-1.08	-3.58	2.5E-03	0.01	2.3E-01
cg05592255	7	99440199	CYP3A43	-1.30	2.0E-10	8.0E-07	-0.94	-2.26	4.9E-02	0.01	2.4E-04
cg08431693	7	99680287	ZNF3	-0.81	4.3E-08	3.2E-05	-0.16	-0.43	4.1E-01	0.00	4.4E-01
cg06193393	7	99869454	GATS	1.16	6.2E-08	4.1E-05	2.61	5.13	3.3E-05	0.00	7.2E-01
cg01754290	7	114066523	FOXP2	0.80	5.7E-09	8.5E-06	-0.59	-0.73	3.4E-01	-0.04	5.4E-18
cg21921829	7	116850153	ST7	-1.18	7.2E-08	4.5E-05	-1.32	-4.45	2.1E-04	0.01	4.2E-03
cg05841967	7	117824643	NAA38	-1.47	4.1E-09	6.8E-06	1.69	3.01	1.0E-02	0.01	7.0E-02
cg06479434	7	128395929	CALU	-1.49	8.3E-08	4.9E-05	-1.63	-3.59	2.4E-03	0.01	4.6E-02
ch.7.2714749F	7	130688396	FLJ43663	1.10	7.4E-08	4.6E-05	2.37	4.38	2.6E-04	-0.01	8.3E-02
cg23013736	7	148584684	EZH2	-2.10	2.3E-12	3.9E-08	-2.14	-2.95	1.2E-02	0.00	2.7E-01
cg25269643	7	151042396	NUB1	-1.56	4.6E-08	3.4E-05	-2.06	-3.94	9.3E-04	0.00	4.2E-01
cg20864326	7	152371422	XRCC2	-1.08	2.4E-09	4.8E-06	-2.22	-3.74	1.6E-03	-0.01	1.2E-01
cg22277672	7	158444325	NCAPG2	-1.27	6.9E-13	1.8E-08	-1.05	-3.81	1.3E-03	0.01	9.1E-02
cg17477493	8	12748272	NA	-1.22	3.4E-10	1.1E-06	-2.03	-4.40	2.5E-04	0.01	9.2E-02
cg18996590	8	30890583	WRN	-1.70	4.2E-09	7.1E-06	-0.39	-0.56	3.8E-01	0.01	5.8E-07
cg18324126	8	30890620	WRN	-1.37	4.1E-10	1.3E-06	0.68	0.91	2.9E-01	0.01	4.2E-03
cg14655858	8	37978472	ASH2L	-1.82	7.7E-09	1.0E-05	-0.49	-0.81	3.2E-01	0.01	5.3E-03
cg18990313	8	38831598	HTRA4	-0.69	8.5E-08	5.0E-05	0.16	0.70	3.5E-01	0.01	3.2E-02
cg09642739	8	42771492	HOOK3	-1.17	9.9E-11	5.0E-07	-0.92	-3.20	6.5E-03	0.01	1.5E-01
cg24555763	8	53300817	ST18	-1.51	1.5E-08	1.6E-05	0.08	0.13	4.9E-01	0.01	4.9E-02
cg12927915	8	66542625	ARMC1	-1.14	5.5E-09	8.3E-06	-1.56	-4.95	5.2E-05	0.01	4.1E-03
cg14783123	8	68022262	CSPP1	1.06	2.1E-08	2.0E-05	-1.31	-1.90	8.9E-02	-0.02	2.1E-07

cg12803724	8	79578360	ZC2HC1A	-1.35	8.5E-08	5.0E-05	-1.33	-2.17	5.8E-02	0.00	3.1E-01
cg13155823	8	80993721	TPD52	-1.47	9.1E-10	2.3E-06	-1.71	-4.79	8.0E-05	0.01	6.2E-04
cg15328990	8	92001646	LOC100127983	0.98	9.4E-12	8.8E-08	-1.03	-3.98	8.3E-04	-0.03	6.1E-10
cg01962989	8	93933251	TRIQK	0.92	1.3E-08	1.4E-05	-1.64	-3.00	1.1E-02	-0.03	7.5E-15
cg16001675	8	95430918	RAD54B	1.28	5.0E-12	6.4E-08	-1.13	-1.23	2.1E-01	-0.03	1.2E-11
cg12861602	8	99045811	MATN2	-0.94	3.3E-08	2.8E-05	-1.01	-3.80	1.4E-03	0.01	3.3E-03
cg00451651	8	100252466	VPS13B	0.67	5.1E-08	3.6E-05	-1.03	-1.77	1.1E-01	-0.04	5.4E-15
cg11882601	8	103524881	NA	-0.99	6.9E-08	4.4E-05	-1.02	-2.23	5.2E-02	0.00	5.6E-01
cg01566592	8	104512858	RIMS2	-1.02	5.9E-08	3.9E-05	0.88	1.50	1.6E-01	0.02	5.3E-05
cg20153124	8	104897821	RIMS2	0.94	4.8E-09	7.8E-06	-0.15	-0.19	4.7E-01	-0.03	2.9E-17
cg01356948	8	116652764	TRPS1	1.63	1.4E-08	1.5E-05	-1.31	-1.58	1.4E-01	-0.01	2.4E-02
cg22721170	8	129141736	NA	-1.03	2.6E-09	5.1E-06	-1.21	-3.12	8.1E-03	0.01	1.7E-01
cg22651271	8	141477422	NA	1.13	7.2E-10	2.0E-06	0.95	2.36	4.0E-02	-0.01	1.6E-01
cg01581024	8	142009794	PTK2	-1.47	3.1E-08	2.6E-05	-0.53	-0.87	3.0E-01	0.01	3.9E-02
cg01296653	9	4678949	CDC37L1	1.31	1.7E-08	1.7E-05	2.09	4.16	5.0E-04	-0.01	2.6E-02
cg13707189	9	19028399	FAM154A	-1.40	1.3E-08	1.5E-05	0.14	0.22	4.6E-01	0.01	2.5E-03
cg14614403	9	20621888	MLLT3	-1.62	1.5E-08	1.6E-05	-2.15	-2.98	1.1E-02	0.01	2.4E-03
cg21246531	9	36039639	RECK	-1.06	1.9E-09	4.1E-06	-1.71	-4.68	1.1E-04	0.01	4.6E-02
cg14569423	9	126523663	DENND1A	-1.29	1.7E-10	7.5E-07	-1.42	-4.93	5.4E-05	0.01	1.5E-02
cg16909341	9	130157113	SLC2A8	-1.11	4.9E-09	7.8E-06	-1.35	-3.24	5.9E-03	0.01	2.0E-02
cg19873199	10	1547478	ADARB2	-1.31	3.3E-08	2.7E-05	-1.16	-1.79	1.0E-01	0.01	1.5E-01
ch.10.202299R	10	6548100	PRKCQ	1.05	6.1E-08	4.0E-05	1.44	2.97	1.1E-02	0.00	5.0E-01
cg16719077	10	7849111	ATP5C1	-1.26	2.5E-09	4.9E-06	-1.52	-4.00	7.9E-04	0.01	3.6E-04
cg07578073	10	11232505	CELF2	-1.06	7.2E-08	4.5E-05	-0.89	-2.70	2.1E-02	0.00	3.4E-01
cg00322919	10	17172000	CUBN	-2.41	3.6E-10	1.1E-06	-1.65	-2.20	5.4E-02	0.00	2.9E-02
cg25248628	10	22518027	NA	-1.30	8.0E-08	4.8E-05	-2.19	-3.58	2.5E-03	0.01	1.3E-05
cg23523755	10	22622459	NA	-1.19	1.4E-09	3.2E-06	-0.29	-0.65	3.6E-01	0.01	4.6E-02
cg23260111	10	46158095	ZFAND4	-1.27	4.9E-10	1.5E-06	-1.29	-4.70	1.0E-04	0.01	3.2E-02
cg02421207	10	64817824	NA	1.36	8.5E-08	5.0E-05	0.79	2.07	6.8E-02	0.00	2.6E-01
cg20278381	10	69682560	HERC4	-1.33	9.8E-08	5.4E-05	-1.32	-2.12	6.2E-02	0.00	2.0E-01
cg26051433	10	75001410	FAM149B1	-1.44	2.6E-08	2.3E-05	-0.66	-1.35	1.9E-01	0.01	8.6E-05
cg26771998	10	75490334	BMS1P4	0.60	3.8E-08	3.0E-05	2.95	5.24	2.5E-05	-0.02	1.3E-04
cg15857152	10	83010483	NA	1.23	1.1E-11	9.9E-08	-1.29	-1.99	7.7E-02	-0.02	2.4E-10
cg13242090	10	97026430	PDLIM1	-1.69	2.0E-10	8.0E-07	0.18	0.32	4.4E-01	0.01	1.9E-02
cg24277876	10	98512183	NA	-0.92	5.9E-09	8.6E-06	-0.71	-1.76	1.1E-01	0.01	2.9E-01
cg26848011	10	101990206	CHUK	-1.67	1.7E-09	3.6E-06	-2.21	-3.38	4.2E-03	0.01	7.2E-02
cg03457345	10	105063519	PCGF6	-1.60	2.2E-09	4.6E-06	-0.87	-1.60	1.4E-01	0.01	3.8E-02
cg01433914	10	111792543	ADD3	-1.59	5.6E-10	1.7E-06	-2.85	-5.58	1.2E-05	0.01	4.8E-03
cg06860555	10	112672711	BBIP1	-1.93	6.8E-09	9.5E-06	-1.51	-2.18	5.7E-02	0.01	7.0E-03
cg26691305	10	112896689	NA	-1.46	7.6E-10	2.0E-06	-0.95	-2.17	5.8E-02	0.00	2.2E-01
cg02571204	10	114591733	NA	-1.54	1.0E-07	5.5E-05	0.63	1.10	2.4E-01	0.00	3.3E-01

cg02309725	10	120454304	CACUL1	-1.29	4.4E-08	3.3E-05	-1.40	-2.45	3.4E-02	0.00	5.4E-01
cg08320413	10	127455161	MMP21	-1.35	2.5E-08	2.3E-05	-1.83	-4.67	1.1E-04	0.01	5.0E-04
cg03539267	10	133823899	NA	-0.69	2.9E-08	2.5E-05	-1.23	-3.50	3.1E-03	0.02	1.2E-02
cg03906820	10	134913608	GPR123	-1.24	2.6E-08	2.4E-05	-1.09	-2.51	3.1E-02	0.00	6.3E-01
cg04880138	11	1007119	AP2A2	-1.29	5.4E-08	3.7E-05	0.31	0.54	3.9E-01	0.01	9.8E-04
cg05834354	11	3116865	OSBPL5	-1.65	1.7E-08	1.7E-05	-0.17	-0.24	4.6E-01	0.01	4.0E-02
cg06127316	11	9599460	WEE1	-0.91	1.9E-08	1.8E-05	-0.57	-2.09	6.6E-02	0.01	2.4E-02
cg13544125	11	14661502	PSMA1	1.53	1.3E-08	1.4E-05	2.32	4.03	7.2E-04	0.00	6.0E-01
cg21107103	11	18630052	SPTY2D1-AS1	-0.94	5.6E-08	3.8E-05	-2.46	-3.75	1.6E-03	0.00	5.5E-01
cg25982561	11	22696308	GAS2	1.64	1.4E-08	1.5E-05	-1.64	-2.14	6.0E-02	-0.01	8.9E-06
cg20749212	11	31262762	NA	0.66	9.2E-08	5.2E-05	-1.97	-3.03	1.0E-02	-0.05	3.8E-20
cg21074594	11	43665775	NA	-0.89	3.3E-08	2.7E-05	2.25	4.11	5.7E-04	0.03	4.1E-14
cg20006187	11	44410456	NA	-1.24	2.1E-08	2.0E-05	-1.93	-3.46	3.4E-03	0.01	1.8E-04
cg10461088	11	47198846	ARFGAP2	1.18	3.7E-08	3.0E-05	-0.62	-1.27	2.0E-01	-0.01	6.4E-05
cg20667822	11	48153832	PTPRJ	-1.40	7.7E-12	8.3E-08	-1.44	-4.37	2.6E-04	0.00	6.9E-01
cg14814018	11	57482501	TMX2-CTNND1	-1.23	2.7E-08	2.4E-05	-1.29	-3.24	5.9E-03	0.01	2.3E-03
cg22838281	11	61133580	CYB561A3	1.50	2.3E-08	2.1E-05	1.09	1.82	1.0E-01	0.00	7.3E-01
cg24829313	11	63684597	RCOR2	1.39	3.0E-09	5.7E-06	1.54	2.32	4.4E-02	-0.01	2.0E-01
cg04519387	11	65556438	OVOL1	-1.09	6.2E-09	8.8E-06	0.11	0.33	4.4E-01	0.00	4.2E-01
cg14908986	11	70120720	PPFIA1	1.40	5.8E-08	3.9E-05	2.58	3.63	2.2E-03	-0.01	5.0E-02
cg22152887	11	72849944	FCHSD2	-1.91	4.6E-08	3.4E-05	-2.40	-4.70	1.0E-04	0.01	4.8E-05
cg03508346	11	89059855	NOX4	0.92	5.7E-09	8.5E-06	-0.92	-1.38	1.8E-01	-0.03	2.0E-11
cg11880242	11	102282062	TMEM123	-3.61	4.7E-12	6.3E-08	-1.42	-1.59	1.4E-01	0.01	1.6E-03
ch.11.2136200F	11	103819223	PDGFD	1.34	2.8E-08	2.5E-05	2.47	3.96	8.8E-04	-0.01	1.8E-03
cg26869362	11	105947257	AASDHPTT	-1.16	5.7E-08	3.8E-05	1.72	3.03	9.9E-03	0.01	1.2E-01
cg13767940	11	111383603	MIR34B	-1.00	1.4E-09	3.2E-06	-0.23	-0.43	4.1E-01	0.01	1.4E-01
cg07258532	11	111640893	PPP2R1B	-1.55	6.1E-09	8.7E-06	-1.31	-3.21	6.4E-03	0.00	1.4E-01
cg14593420	12	1708017	FBXL14	-1.61	1.1E-08	1.3E-05	0.78	1.21	2.2E-01	0.01	1.1E-01
cg19264056	12	20704653	PDE3A	1.47	1.3E-10	6.0E-07	-2.43	-2.20	5.5E-02	-0.02	3.7E-15
cg14525610	12	20848821	SLCO1C1	0.97	6.0E-09	8.7E-06	-1.64	-3.04	9.7E-03	-0.03	5.7E-13
cg20251156	12	55793381	OR6C65	1.07	3.8E-09	6.5E-06	-2.41	-3.71	1.8E-03	-0.03	3.3E-14
cg22473961	12	56119258	CD63	-1.12	4.4E-08	3.3E-05	-1.09	-3.46	3.4E-03	0.01	6.4E-05
cg27458327	12	56878323	GLS2	-1.22	1.7E-10	7.5E-07	-0.82	-1.46	1.6E-01	0.00	5.8E-01
cg07933493	12	57345934	RDH16	-1.67	9.5E-08	5.3E-05	-0.88	-1.70	1.2E-01	0.01	7.5E-03
cg11806823	12	60812268	NA	0.62	2.0E-09	4.3E-06	-1.13	-2.02	7.4E-02	-0.06	1.3E-21
cg00089798	12	62585204	FAM19A2	-1.21	1.4E-08	1.5E-05	-0.11	-0.35	4.3E-01	0.01	8.6E-02
cg24476842	12	72179582	RAB21	1.14	1.0E-07	5.5E-05	-1.47	-2.11	6.3E-02	-0.02	6.4E-10
cg11505180	12	75724112	CAPS2	-1.58	1.7E-08	1.7E-05	-1.94	-2.84	1.5E-02	0.01	2.6E-07
cg19430489	12	75728104	GLIPR1L1	-0.85	4.3E-12	6.3E-08	0.44	1.06	2.6E-01	0.05	6.3E-15
cg07684809	12	75728212	GLIPR1L1	-1.08	9.1E-11	4.7E-07	0.09	0.16	4.8E-01	0.03	8.2E-15
cg02921003	12	75728281	GLIPR1L1	-0.80	9.4E-08	5.3E-05	-0.47	-0.79	3.2E-01	0.03	8.0E-13

cg23828765	12	78340971	NAV3	0.67	7.7E-08	4.7E-05	-2.12	-3.39	4.1E-03	-0.04	7.2E-16
cg05708079	12	90102477	LINC00936	-1.26	2.8E-08	2.5E-05	-1.49	-1.84	9.7E-02	0.01	5.3E-02
cg13425650	12	94093761	CRADD	-1.44	2.4E-10	9.0E-07	-1.52	-4.10	5.9E-04	0.02	8.6E-07
cg27129363	12	95376814	NDUFA12	2.00	4.2E-08	3.2E-05	0.44	0.67	3.5E-01	0.00	4.1E-01
cg19860663	12	117348460	FBXW8	1.40	2.5E-10	9.3E-07	0.86	1.81	1.0E-01	-0.02	1.9E-07
cg07718303	12	121261039	SPPL3	-1.58	3.5E-13	1.1E-08	-1.13	-2.67	2.2E-02	0.00	3.9E-01
cg06657560	12	121841372	RNF34	-1.77	5.6E-10	1.7E-06	-0.87	-1.27	2.0E-01	0.00	3.3E-01
cg12906108	12	124284083	DNAH10	-2.44	3.6E-14	3.3E-09	-2.53	-2.46	3.4E-02	0.00	6.4E-01
cg27505193	12	124946377	NCOR2	-1.54	7.5E-10	2.0E-06	-1.95	-2.74	1.9E-02	0.01	1.0E-04
cg25282652	12	128364739	FLJ37505	-1.09	5.1E-08	3.6E-05	-1.79	-4.17	4.8E-04	0.01	1.6E-01
cg11496226	12	129571803	TMEM132D	-1.73	3.2E-08	2.7E-05	-2.39	-3.35	4.5E-03	0.00	9.0E-02
cg01259104	12	133340965	ANKLE2	2.07	6.1E-08	4.0E-05	-2.87	-2.57	2.7E-02	0.01	6.0E-04
cg08741809	13	20527552	NA	-1.46	6.5E-12	7.3E-08	-1.14	-3.20	6.6E-03	0.00	3.7E-01
cg05099186	13	39923838	LHFP	1.77	2.2E-10	8.5E-07	2.22	4.31	3.2E-04	0.00	7.2E-01
cg14792031	13	41707137	KBTBD6	1.08	1.3E-08	1.4E-05	1.12	2.42	3.7E-02	-0.01	1.4E-01
cg09814151	13	45151437	TSC22D1	-1.19	8.4E-08	4.9E-05	1.23	2.24	5.1E-02	0.01	1.3E-01
cg02593615	13	45918202	TPT1-AS1	-1.44	5.7E-08	3.9E-05	-0.89	-1.54	1.5E-01	0.00	3.3E-01
cg25399333	13	50856824	NA	-1.60	1.2E-08	1.4E-05	-2.19	-3.37	4.3E-03	0.00	2.1E-01
cg08866608	13	58203798	PCDH17	-1.03	2.1E-10	8.1E-07	2.69	5.11	3.5E-05	0.02	6.4E-05
cg25543578	13	62516040	NA	1.32	5.6E-09	8.4E-06	0.23	0.30	4.5E-01	-0.01	4.1E-06
cg01075555	13	63264349	NA	0.71	3.1E-08	2.6E-05	-2.42	-4.24	3.9E-04	-0.04	1.0E-14
cg00603225	13	65724231	NA	1.31	2.4E-08	2.2E-05	0.63	0.74	3.4E-01	-0.01	4.8E-07
cg18041207	13	72441404	DACH1	-1.33	3.3E-09	5.9E-06	1.14	2.25	5.0E-02	0.01	3.4E-02
cg04139515	13	78272639	SLAIN1	-0.77	5.3E-08	3.7E-05	-1.87	-3.45	3.5E-03	0.02	1.7E-03
cg16574347	13	78327370	SLAIN1	-1.73	1.2E-08	1.4E-05	-2.21	-3.55	2.7E-03	0.01	1.5E-02
cg02704594	13	82264029	NA	0.75	2.8E-08	2.5E-05	-1.20	-1.93	8.5E-02	-0.04	1.1E-15
cg12206423	13	88330614	SLITRK5	-0.89	3.2E-10	1.1E-06	-0.36	-1.13	2.4E-01	0.01	2.0E-01
cg15470836	13	100648306	NA	1.19	8.3E-08	4.9E-05	0.81	1.59	1.4E-01	-0.01	2.1E-02
cg09626833	13	113174173	TUBGCP3	-1.39	3.7E-09	6.3E-06	-0.07	-0.17	4.8E-01	0.01	7.7E-03
cg26995035	13	113785830	F10	-1.31	4.7E-08	3.4E-05	-1.14	-3.29	5.2E-03	0.01	2.3E-02
cg18462916	13	113918539	CUL4A	-1.52	7.8E-08	4.8E-05	-1.74	-4.31	3.2E-04	0.01	1.2E-04
cg07010207	14	21238111	EDDM3B	-1.50	5.9E-08	3.9E-05	-0.98	-2.73	1.9E-02	0.01	6.8E-03
cg13979573	14	21584590	NA	-1.80	7.9E-11	4.1E-07	-1.45	-4.26	3.7E-04	0.01	8.7E-05
cg17002899	14	21727471	HNRNPC	1.94	2.2E-09	4.5E-06	1.01	1.42	1.7E-01	0.00	9.3E-02
cg27020028	14	23304823	MMP14	1.25	6.8E-08	4.3E-05	-0.68	-1.20	2.2E-01	0.00	6.4E-01
cg11720863	14	24604040	PSME1	-1.49	8.4E-10	2.1E-06	-2.08	-3.61	2.3E-03	0.01	1.6E-02
cg19707326	14	24787611	ADCY4	1.83	4.9E-08	3.5E-05	-0.29	-0.57	3.8E-01	0.00	3.7E-01
cg05224124	14	35583718	PPP2R3C	-1.47	4.7E-12	6.3E-08	-1.26	-3.04	9.6E-03	0.02	5.0E-08
cg19668728	14	53907837	NA	-1.41	7.3E-08	4.6E-05	-1.70	-3.21	6.4E-03	0.01	4.0E-06
cg23173466	14	65565498	MAX	0.93	3.7E-08	2.9E-05	1.59	3.50	3.0E-03	0.00	7.3E-01
cg16709294	14	70235567	LOC100289511	-1.97	5.8E-08	3.9E-05	1.04	0.95	2.8E-01	0.00	4.5E-01

cg21507487	14	71941057	NA	-1.47	5.8E-10	1.7E-06	-0.83	-2.60	2.5E-02	0.01	4.9E-04
cg05180258	14	73921198	NUMB	-1.08	3.8E-11	2.4E-07	-1.52	-4.53	1.7E-04	0.01	2.3E-02
cg11697159	14	89259164	EML5	-1.27	9.6E-08	5.4E-05	1.22	1.35	1.9E-01	0.01	5.9E-04
cg24156331	14	93430253	ITPK1	-1.16	1.7E-13	7.0E-09	-0.64	-1.65	1.3E-01	0.02	7.1E-03
cg07093953	14	101004930	BEGAIN	-1.48	8.3E-08	4.9E-05	-0.92	-1.74	1.1E-01	0.01	3.5E-02
cg13153796	14	101405628	SNORD113-6	0.85	1.2E-08	1.4E-05	0.96	1.14	2.3E-01	-0.03	4.7E-13
cg17930169	14	101406815	SNORD113-7	0.55	1.0E-08	1.3E-05	-1.01	-1.87	9.3E-02	-0.05	1.2E-11
cg10245797	14	101437325	SNORD114-13	0.88	3.1E-08	2.6E-05	-1.72	-1.99	7.7E-02	-0.04	4.5E-19
cg24165760	14	103243389	TRAF3	-2.07	6.3E-10	1.8E-06	-0.93	-1.41	1.8E-01	0.00	1.9E-01
cg22731164	15	40192158	GPR176	-1.68	1.4E-08	1.5E-05	-2.19	-4.23	4.0E-04	0.00	2.1E-01
cg25217313	15	41624774	OIP5	-1.79	5.5E-08	3.7E-05	-2.39	-3.45	3.5E-03	0.01	2.4E-03
cg10517312	15	45027253	TRIM69	2.01	2.4E-08	2.2E-05	0.27	0.77	3.3E-01	-0.01	6.1E-03
cg10542300	15	48442807	MYEF2	0.62	5.8E-08	3.9E-05	-2.04	-3.72	1.7E-03	-0.04	1.2E-13
cg22700091	15	48470612	MYEF2	-1.36	4.1E-08	3.2E-05	1.52	2.14	6.1E-02	0.01	1.2E-04
cg25951582	15	49913451	DTWD1	-1.33	5.4E-08	3.7E-05	-0.54	-1.03	2.6E-01	0.01	1.1E-02
cg13402936	15	50471108	SLC27A2	-1.64	1.1E-13	5.2E-09	-2.29	-4.86	6.6E-05	0.01	4.1E-03
cg04474209	15	52484920	GNB5	-0.95	8.1E-08	4.9E-05	-1.60	-5.28	2.3E-05	0.01	2.5E-03
cg01834151	15	52971181	FAM214A	-1.43	6.6E-10	1.8E-06	0.28	0.51	3.9E-01	0.01	5.2E-05
cg02539984	15	58960059	ADAM10	1.20	7.8E-08	4.8E-05	-3.30	-4.87	6.4E-05	-0.02	1.8E-08
cg03850730	15	62531125	NA	1.34	3.5E-08	2.8E-05	-0.17	-0.31	4.4E-01	-0.01	1.4E-01
cg04258046	15	63445591	RPS27L	-1.12	1.1E-08	1.3E-05	-1.56	-4.61	1.4E-04	0.01	1.3E-01
cg11741168	15	64673872	KIAA0101	1.14	7.2E-08	4.5E-05	1.42	2.79	1.7E-02	-0.01	7.1E-05
cg21527414	15	65906825	VWA9	-1.41	4.7E-08	3.4E-05	-0.96	-1.48	1.6E-01	0.00	3.3E-01
cg20566885	15	70995014	UACA	1.25	1.5E-10	7.0E-07	-1.29	-1.87	9.4E-02	-0.02	2.1E-11
cg04813639	15	79383947	RASGRF1	-1.02	1.7E-08	1.7E-05	0.12	0.23	4.6E-01	0.01	2.5E-01
cg12651540	15	90191926	KIF7	1.60	8.8E-09	1.2E-05	0.30	0.36	4.3E-01	-0.01	3.9E-06
cg02320474	16	1758022	MAPK8IP3	-0.80	1.5E-08	1.6E-05	-0.49	-1.90	9.0E-02	0.00	4.8E-01
cg10293804	16	3068529	CLDN6	-0.84	3.5E-08	2.8E-05	-0.91	-2.82	1.6E-02	0.01	2.2E-01
cg00086426	16	10934373	NA	-1.04	7.9E-08	4.8E-05	-1.20	-3.18	7.0E-03	0.01	5.7E-03
cg06183001	16	48406857	MIR548AE2	-1.83	4.3E-11	2.6E-07	-0.43	-0.66	3.6E-01	0.00	5.4E-01
cg04939900	16	48411586	MIR548AE2	-1.51	9.6E-08	5.4E-05	-1.82	-2.98	1.1E-02	0.01	6.2E-03
cg02550308	16	69310261	SNTB2	-1.75	3.2E-09	5.8E-06	-2.16	-3.30	5.1E-03	0.00	3.1E-01
cg01695579	16	70571479	SNORD111	-2.64	5.5E-14	3.8E-09	-1.02	-1.42	1.7E-01	0.00	5.6E-02
cg01442398	16	80838258	CDYL2	-1.26	5.4E-09	8.2E-06	-1.23	-2.26	4.9E-02	0.00	4.1E-01
cg07700920	16	84780726	USP10	-2.44	3.1E-09	5.8E-06	-0.59	-0.90	2.9E-01	0.00	5.6E-02
cg16743903	16	89593216	SPG7	-1.54	2.3E-08	2.1E-05	-2.11	-4.38	2.6E-04	0.01	3.7E-08
cg01717881	17	122697	RPH3AL	-1.67	4.5E-09	7.5E-06	-0.80	-1.18	2.3E-01	0.01	5.9E-03
cg00752045	17	2588136	PAFAH1B1	-1.30	2.0E-10	8.0E-07	-0.97	-2.17	5.8E-02	0.01	1.3E-01
cg01940508	17	5185538	RABEP1	-1.42	1.9E-08	1.8E-05	-1.25	-1.98	7.8E-02	0.01	1.4E-02
cg16118259	17	5316884	NUP88	-1.13	1.7E-09	3.7E-06	-0.87	-2.56	2.8E-02	0.01	1.2E-03
cg02704946	17	6527184	KIAA0753	-1.71	3.4E-08	2.8E-05	-2.26	-4.22	4.2E-04	0.01	7.0E-05

cg08460590	17	7495881	SOX15	-1.11	1.6E-08	1.6E-05	-0.88	-2.29	4.6E-02	0.01	1.2E-01
cg01691987	17	7789028	CHD3	-0.98	4.6E-08	3.4E-05	-1.86	-3.83	1.3E-03	0.01	6.6E-02
cg09186482	17	8082780	TMEM107	-1.43	6.9E-08	4.4E-05	-1.74	-3.26	5.7E-03	0.01	3.4E-02
cg04195226	17	16158686	PIGL	-1.16	5.3E-08	3.7E-05	-1.62	-3.12	8.0E-03	0.01	2.5E-01
cg14640532	17	16880871	NA	-1.75	1.0E-07	5.5E-05	1.02	1.33	1.9E-01	0.00	8.3E-02
cg04864152	17	19247902	MIR1180	-1.33	2.3E-08	2.2E-05	-1.79	-3.05	9.4E-03	0.01	9.3E-02
cg14868594	17	19913217	SPECC1	-1.00	3.4E-08	2.8E-05	-0.68	-1.25	2.1E-01	0.01	1.2E-03
cg03117577	17	20187457	SPECC1	1.61	3.5E-10	1.1E-06	2.60	3.87	1.1E-03	-0.01	3.3E-02
cg09818637	17	20683924	NA	1.90	5.4E-11	3.2E-07	0.68	1.10	2.4E-01	0.01	1.6E-02
cg03218192	17	33914403	AP2B1	1.37	7.6E-08	4.7E-05	-4.13	-3.34	4.7E-03	-0.01	2.1E-11
cg02782889	17	47074637	IGF2BP1	-0.63	5.3E-08	3.7E-05	-1.20	-2.24	5.1E-02	0.02	2.0E-04
cg13894852	17	47502298	NA	-0.78	1.8E-08	1.8E-05	NA	NA	NA	0.02	4.0E-03
cg27657459	17	54853771	NA	-1.32	8.6E-12	8.4E-08	-1.72	-5.76	9.0E-06	0.02	9.4E-06
cg09628499	17	56299729	MKS1	-1.50	8.3E-13	1.9E-08	-1.57	-4.35	2.9E-04	0.01	1.7E-04
cg02656609	17	57228618	MIR301A	-1.61	3.7E-09	6.3E-06	-1.73	-2.58	2.6E-02	0.00	1.3E-01
cg17945004	17	58984873	BCAS3	1.25	1.7E-08	1.7E-05	-1.19	-1.55	1.5E-01	-0.02	9.1E-10
cg00221096	17	67312052	ABCA5	1.30	6.4E-09	9.2E-06	-1.25	-1.92	8.7E-02	-0.02	6.2E-09
cg07899956	17	74261249	UBALD2	0.94	8.2E-08	4.9E-05	1.03	1.55	1.5E-01	0.00	7.3E-01
cg04256065	17	76102509	TNRC6C	-1.45	8.2E-08	4.9E-05	-3.45	-4.02	7.4E-04	0.00	7.0E-01
cg10473821	17	80894243	TBCD	-1.75	5.2E-09	8.0E-06	-0.40	-0.61	3.7E-01	0.01	5.5E-03
cg12105108	18	2571648	NDC80	-1.40	1.4E-09	3.2E-06	-0.13	-0.22	4.7E-01	0.01	4.7E-03
cg16954236	18	8638786	RAB12	-1.39	3.5E-11	2.4E-07	-1.60	-4.92	5.6E-05	0.01	2.3E-03
cg23419170	18	12067067	NA	3.30	3.7E-08	2.9E-05	4.29	3.42	3.8E-03	0.00	9.9E-04
cg20034091	18	31158527	ASXL3	-1.42	1.1E-12	2.1E-08	-0.51	-0.92	2.9E-01	0.01	2.8E-05
cg12361352	18	31158540	ASXL3	-1.20	8.8E-13	1.9E-08	-1.63	-3.96	8.8E-04	0.02	3.8E-07
cg27109877	18	31158549	ASXL3	-1.12	3.5E-10	1.1E-06	-0.40	-1.12	2.4E-01	0.02	2.1E-05
ch.18.658499F	18	33592866	RPRD1A	1.23	8.7E-08	5.1E-05	1.18	2.68	2.2E-02	-0.01	6.7E-02
cg09730015	18	43914047	RNF165	-0.91	3.5E-09	6.1E-06	-1.13	-2.62	2.5E-02	0.00	4.5E-01
cg05692899	18	77342368	NA	-2.54	3.0E-10	1.1E-06	-2.69	-3.52	2.9E-03	0.01	2.3E-06
cg27172769	19	1255283	MIDN	2.15	1.7E-08	1.7E-05	-1.43	-1.40	1.8E-01	0.00	1.9E-01
cg05348870	19	6671045	TNFSF14	-2.33	1.1E-09	2.6E-06	-1.60	-2.36	4.1E-02	0.01	7.6E-07
cg12085704	19	12774100	MAN2B1	1.70	9.8E-08	5.4E-05	0.43	0.62	3.7E-01	0.00	1.6E-01
cg18569070	19	17136562	CPAMD8	-1.75	1.9E-08	1.8E-05	-2.69	-5.47	1.5E-05	0.01	2.7E-04
cg10812466	19	32718114	NA	-1.21	2.4E-08	2.2E-05	-1.60	-3.81	1.3E-03	0.01	1.6E-02
cg24757346	19	35629022	FXYD1	-1.73	1.0E-07	5.5E-05	-1.71	-2.36	4.1E-02	0.01	1.7E-03
cg06632759	19	37702089	ZNF585B	-1.60	3.7E-11	2.4E-07	-2.59	-4.61	1.4E-04	0.02	4.4E-07
cg04614760	19	40022828	EID2B	-1.09	5.4E-08	3.7E-05	-0.22	-0.71	3.4E-01	0.00	6.4E-01
cg00498691	19	40315143	NA	-0.95	3.5E-08	2.8E-05	-0.32	-0.58	3.8E-01	0.00	6.1E-01
cg02474193	19	41630546	CYP2F1	2.06	4.7E-08	3.4E-05	-1.06	-1.07	2.5E-01	0.00	2.2E-01
cg13596036	19	41773743	HNRNPUL1	1.75	7.3E-09	1.0E-05	0.83	1.48	1.6E-01	-0.01	5.8E-03
cg26985354	19	45567180	CLASRP	1.13	7.2E-11	3.9E-07	0.21	0.37	4.3E-01	0.02	2.0E-04

cg02679291	19	48248902	GLTSCR2	1.90	3.5E-08	2.8E-05	4.73	4.88	6.3E-05	-0.01	1.6E-04
cg01139412	19	50316597	FUZ	1.88	1.3E-10	6.1E-07	-0.61	-0.92	2.9E-01	-0.01	2.3E-02
cg09374437	19	52769790	ZNF766	-1.61	6.4E-10	1.8E-06	-0.83	-1.69	1.2E-01	0.01	3.0E-04
cg08355109	19	56599667	ZNF787	2.01	4.1E-08	3.2E-05	-2.48	-2.06	6.9E-02	-0.01	8.3E-04
cg18748575	20	400950	RBCK1	1.96	2.6E-08	2.4E-05	1.03	1.86	9.5E-02	0.00	4.5E-01
cg13403466	20	1444630	NSFL1C	-1.80	1.0E-11	9.3E-08	-1.25	-3.35	4.6E-03	0.02	1.6E-11
cg23032598	20	17512795	BFSP1	-1.08	4.2E-08	3.2E-05	-0.95	-2.44	3.5E-02	0.01	2.6E-01
cg19115692	20	34209773	NA	-1.84	7.7E-10	2.0E-06	-0.50	-0.81	3.2E-01	0.01	9.0E-05
cg02672530	20	34680964	EPB41L1	-0.64	1.2E-08	1.4E-05	-1.29	-2.63	2.4E-02	0.01	1.5E-01
cg03819338	20	39942766	NA	-2.03	4.2E-11	2.6E-07	-1.16	-2.34	4.2E-02	0.01	2.9E-02
cg02555585	20	42090853	SRSF6	-1.20	5.5E-08	3.7E-05	0.18	0.30	4.5E-01	0.00	6.1E-01
cg27150417	20	44462035	SNX21	-0.84	7.7E-08	4.7E-05	-0.14	-0.64	3.6E-01	0.01	1.6E-01
cg12751354	20	52770785	CYP24A1	-1.07	7.0E-08	4.4E-05	-1.20	-3.12	8.1E-03	0.01	1.5E-01
cg25325053	20	58533022	CDH26	-1.64	3.5E-08	2.8E-05	-2.02	-3.49	3.1E-03	0.00	5.1E-01
cg02296167	20	62363890	LIME1	-1.22	5.8E-08	3.9E-05	-1.51	-2.54	2.8E-02	0.01	7.5E-06
cg11433319	21	19617873	CHODL	-1.28	9.5E-08	5.3E-05	2.51	3.73	1.7E-03	0.01	2.4E-02
cg17297071	21	26934424	MIR155HG	-1.18	5.5E-08	3.7E-05	-0.94	-1.56	1.4E-01	0.01	2.1E-02
cg23508786	21	34775291	IFNGR2	-1.14	7.5E-10	2.0E-06	-1.18	-2.78	1.7E-02	0.01	2.3E-01
cg19325435	22	22839645	ZNF280B	-1.58	5.2E-08	3.7E-05	-1.48	-2.43	3.6E-02	0.01	4.3E-02
cg24062706	22	30658924	OSM	1.08	3.5E-08	2.8E-05	1.78	2.94	1.2E-02	0.00	3.3E-01
cg05080787	22	50277948	ZBED4	-1.77	3.2E-09	5.8E-06	0.77	1.26	2.1E-01	0.01	3.8E-04
cg01162841	X	19818905	SH3KBP1	-1.40	4.3E-08	3.2E-05	-1.59	-3.82	1.3E-03	0.01	3.7E-05
cg16576300	X	64136881	ZC4H2	0.93	9.0E-08	5.2E-05	0.45	1.19	2.2E-01	0.00	6.8E-01
cg23522780	X	118712792	UBE2A	-1.17	2.4E-09	4.7E-06	-1.92	-5.09	3.6E-05	0.01	4.2E-03

\* Listed are the dmCpGs identified from Sister Study dataset at P value threshold of  $1 \times 10^{-7}$ .  
Abbreviations: Sister Study (SS); EPIC-Italy Study (EPIC); time to diagnosis (t2d); coefficient (coef).

**Supplementary Table 2.** Gene pathway analysis result for the 2,095 differentially methylated CpGs identified for breast cancer\*

IPAid	p_simu	Pathway Category
Lymphotoxin $\beta^2$ Receptor Signaling	0.023	Apoptosis
JAK/Stat Signaling	0.005	Apoptosis, Cellular Growth, Proliferation and Development, Intracellular and Second Messenger Signaling
IL-9 Signaling	0.024	Apoptosis, Cellular Immune Response, Cytokine Signaling
LPS-stimulated MAPK Signaling	0.025	Apoptosis, Pathogen-Influenced Signaling
Telomerase Signaling	0.001	Cancer, Apoptosis
PTEN Signaling	0.016	Cancer, Apoptosis
FAK Signaling	0.014	Cancer, Cellular Growth, Proliferation and Development
PI3K/AKT Signaling	0.004	Cancer, Cellular Growth, Proliferation and Development, Intracellular and Second Messenger Signaling
Role of BRCA1 in DNA Damage Response	0.002	Cancer, Cellular Stress and Injury
Melanoma Signaling	0.004	Cancer, Disease-Specific Pathways
Endometrial Cancer Signaling	0.004	Cancer, Disease-Specific Pathways
Estrogen-Dependent Breast Cancer Signaling	0.007	Cancer, Disease-Specific Pathways
Acute Myeloid Leukemia Signaling	0.010	Cancer, Disease-Specific Pathways
Chronic Myeloid Leukemia Signaling	0.025	Cancer, Disease-Specific Pathways
Prostate Cancer Signaling	0.002	Cancer, Disease-Specific Pathways
Hereditary Breast Cancer Signaling	0.009	Cancer, Disease-Specific Pathways
Glioma Signaling	0.002	Cancer, Disease-Specific Pathways
Glioblastoma Multiforme Signaling	0.007	Cancer, Disease-Specific Pathways
Ovarian Cancer Signaling	0.001	Cancer, Disease-Specific Pathways
Breast Cancer Regulation by Stathmin1	0.004	Cancer, Disease-Specific Pathways
Molecular Mechanisms of Cancer	0.041	Cancer, Disease-Specific Pathways
p53 Signaling	0.010	Cancer, Ingenuity Toxicity List Pathways
Cancer Drug Resistance By Drug Efflux	0.022	Cancer, Ingenuity Toxicity List Pathways, Xenobiotic Metabolism
ERK/MAPK Signaling	0.014	Cancer, Intracellular and Second Messenger Signaling
Wnt/ $\beta^2$ -catenin Signaling	0.004	Cancer, Organismal Growth and Development
Inhibition of Angiogenesis by TSP1	0.006	Cardiovascular Signaling

Nitric Oxide Signaling in the Cardiovascular System	0.016	Cardiovascular Signaling
P2Y Purigenic Receptor Signaling Pathway	0.034	Cardiovascular Signaling
Thrombin Signaling	0.032	Cardiovascular Signaling
Cardiac Hypertrophy Signaling	0.047	Cardiovascular Signaling,Disease-Specific Pathways
Renin-Angiotensin Signaling	0.018	Cardiovascular Signaling,Growth Factor Signaling
Mitotic Roles of Polo-Like Kinase	0.002	Cell Cycle Regulation
Antiproliferative Role of Somatostatin Receptor 2	0.036	Cell Cycle Regulation
Ceramide Signaling	0.006	Cell Cycle Regulation,Apoptosis
14-3-3-mediated Signaling	0.022	Cell Cycle Regulation,Apoptosis
Tight Junction Signaling	0.017	Cell Cycle Regulation,Apoptosis
Integrin Signaling	0.042	Cell Cycle Regulation,Cellular Growth, Proliferation and Development,Intracellular and Second Messenger Signaling
Role of CHK Proteins in Cell Cycle Checkpoint Control	0.004	Cell Cycle Regulation,Cellular Stress and Injury
Thrombopoietin Signaling	0.019	Cellular Growth, Proliferation and Development
PEDF Signaling	0.004	Cellular Growth, Proliferation and Development
Gap Junction Signaling	0.002	Cellular Growth, Proliferation and Development
GM-CSF Signaling	0.011	Cellular Growth, Proliferation and Development,Cellular Immune Response,Cytokine Signaling,Growth Factor Signaling
p70S6K Signaling	<0.001	Cellular Growth, Proliferation and Development,Cellular Stress and Injury
Regulation of eIF4 and p70S6K Signaling	0.014	Cellular Growth, Proliferation and Development,Cellular Stress and Injury,Intracellular and Second Messenger Signaling
RANK Signaling in Osteoclasts	0.015	Cellular Growth, Proliferation and Development,Disease-Specific Pathways
VEGF Family Ligand-Receptor Interactions	0.027	Cellular Growth, Proliferation and Development,Growth Factor Signaling
Erythropoietin Signaling	0.027	Cellular Growth, Proliferation and Development,Growth Factor Signaling
Growth Hormone Signaling	0.033	Cellular Growth, Proliferation and Development,Growth Factor Signaling
PDGF Signaling	0.029	Cellular Growth, Proliferation and Development,Growth Factor Signaling
VEGF Signaling	0.011	Cellular Growth, Proliferation and Development,Growth Factor Signaling
IGF-1 Signaling	0.001	Cellular Growth, Proliferation and Development,Growth Factor Signaling
HGF Signaling	0.024	Cellular Growth, Proliferation and Development,Growth Factor Signaling,Organismal Growth and Development

AMPK Signaling	0.036	Cellular Growth, Proliferation and Development, Intracellular and Second Messenger Signaling
Mouse Embryonic Stem Cell Pluripotency	0.016	Cellular Growth, Proliferation and Development, Organismal Growth and Development
CD28 Signaling in T Helper Cells	0.023	Cellular Immune Response
Natural Killer Cell Signaling	0.018	Cellular Immune Response
CTLA4 Signaling in Cytotoxic T Lymphocytes	0.008	Cellular Immune Response
T Cell Receptor Signaling	0.005	Cellular Immune Response
Leukocyte Extravasation Signaling	0.003	Cellular Immune Response
Production of Nitric Oxide and Reactive Oxygen Species in Macrophages	0.003	Cellular Immune Response
IL-2 Signaling	0.028	Cellular Immune Response, Cytokine Signaling
IL-3 Signaling	0.018	Cellular Immune Response, Cytokine Signaling
CCR3 Signaling in Eosinophils	0.016	Cellular Immune Response, Cytokine Signaling
fMLP Signaling in Neutrophils	0.007	Cellular Immune Response, Cytokine Signaling
CXCR4 Signaling	0.029	Cellular Immune Response, Cytokine Signaling
IL-8 Signaling	0.006	Cellular Immune Response, Cytokine Signaling
NF- $\kappa$ B Signaling	0.037	Cellular Immune Response, Cytokine Signaling, Humoral Immune Response, Ingenuity Toxicity List Pathways, Organismal Growth and Development
Clathrin-mediated Endocytosis Signaling	0.038	Cellular Immune Response, Organismal Growth and Development, Pathogen-Influenced Signaling
Role of Pattern Recognition Receptors in Recognition of Bacteria and Viruses	<0.001	Cellular Immune Response, Pathogen-Influenced Signaling
NF- $\kappa$ B Activation by Viruses	0.013	Cellular Immune Response, Pathogen-Influenced Signaling
Type II Diabetes Mellitus Signaling	0.008	Cellular Stress and Injury, Disease-Specific Pathways
NRF2-mediated Oxidative Stress Response	0.019	Cellular Stress and Injury, Ingenuity Toxicity List Pathways
IL-17A Signaling in Airway Cells	0.011	Cytokine Signaling
Chemokine Signaling	0.047	Cytokine Signaling, Organismal Growth and Development
Prolactin Signaling	0.004	Cytokine Signaling, Organismal Growth and Development
Role of Wnt/GSK-3 $\beta$ Signaling in the Pathogenesis of Influenza	0.024	Disease-Specific Pathways, Pathogen-Influenced Signaling
ErbB2-ErbB3 Signaling	0.027	Growth Factor Signaling, Neurotransmitters and Other Nervous System Signaling
ErbB4 Signaling	0.021	Growth Factor Signaling, Neurotransmitters and Other Nervous System Signaling

NGF Signaling	0.046	Growth Factor Signaling, Neurotransmitters and Other Nervous System Signaling
Relaxin Signaling	0.050	Growth Factor Signaling, Organismal Growth and Development
Fc Epsilon RI Signaling	0.016	Humoral Immune Response
Xenobiotic Metabolism Signaling	0.005	Ingenuity Toxicity List Pathways, Xenobiotic Metabolism
G $\pm$ 12/13 Signaling	0.024	Intracellular and Second Messenger Signaling
Rac Signaling	0.031	Intracellular and Second Messenger Signaling
Sphingosine-1-phosphate Signaling	0.023	Intracellular and Second Messenger Signaling
Insulin Receptor Signaling	0.004	Intracellular and Second Messenger Signaling
Protein Ubiquitination Pathway	0.047	Intracellular and Second Messenger Signaling
Glucocorticoid Receptor Signaling	0.038	Intracellular and Second Messenger Signaling
G $\pm$ q Signaling	0.002	Intracellular and Second Messenger Signaling
Protein Kinase A Signaling	0.035	Intracellular and Second Messenger Signaling
Dopamine-DARPP32 Feedback in cAMP Signaling	0.019	Intracellular and Second Messenger Signaling, Neurotransmitters and Other Nervous System Signaling
Melatonin Signaling	0.037	Neurotransmitters and Other Nervous System Signaling
Cholecystokinin/Gastrin-mediated Signaling	0.049	Neurotransmitters and Other Nervous System Signaling
Ephrin A Signaling	0.035	Neurotransmitters and Other Nervous System Signaling, Organismal Growth and Development
Ephrin B Signaling	0.008	Neurotransmitters and Other Nervous System Signaling, Organismal Growth and Development
Ephrin Receptor Signaling	0.039	Neurotransmitters and Other Nervous System Signaling, Organismal Growth and Development
HIPPO signaling	0.015	Organismal Growth and Development
Actin Cytoskeleton Signaling	0.009	Organismal Growth and Development
Regulation of the Epithelial-Mesenchymal Transition Pathway	0.008	Organismal Growth and Development
Virus Entry via Endocytic Pathways	0.025	Pathogen-Influenced Signaling
Sumoylation Pathway	0.041	Transcriptional Regulation, Cellular Growth, Proliferation and Development, Cellular Stress and Injury
Role of NANOG in Mammalian Embryonic Stem Cell Pluripotency	0.011	Transcriptional Regulation, Cellular Growth, Proliferation and Development, Organismal Growth and Development

\* Listed are the enriched canonical IPA (Ingenuity Pathway Analysis) signaling pathways at permutation P value threshold of 0.05.

**Supplementary Table 3.** Overlap between genes identified by previous GWAS studies (<https://www.ebi.ac.uk/gwas/>) and genes with differentially methylated CpGs in our study\*

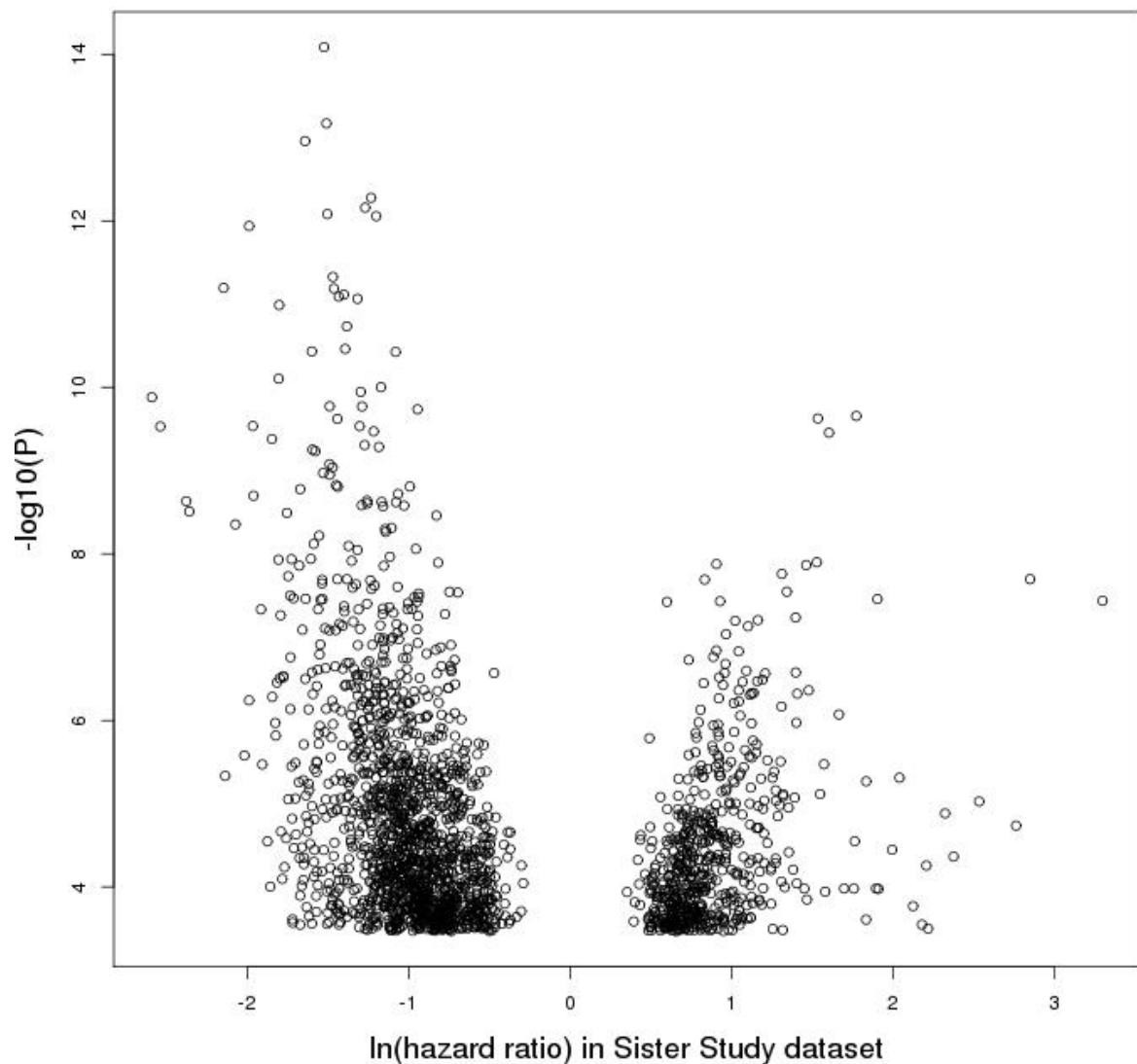
probe	gene	coef_SS	q_SS	coef_EPIC	q_EPIC
cg14569423	DENND1A	-1.29	7.46E-07	-1.42	5.41E-05
cg23123909	RAB3C	-1.49	7.46E-07	-1.45	7.10E-03
cg13155823	TPD52	-1.47	2.32E-06	-1.71	7.95E-05
cg09664975	PRKACB	-0.83	6.08E-06	-2.07	4.06E-04
cg07768372	TRIO	-1.78	1.17E-04	-3.38	2.55E-04
cg18814252	BCL9	-0.93	1.21E-04	-1.58	8.69E-05
cg10155725	ME3	-0.71	3.42E-04	-1.03	2.14E-03
cg21681962	ATM	-1.41	7.58E-04	-2.68	2.33E-03
cg07619683	ESR1	-1.10	9.99E-04	-2.08	5.88E-05
cg23713965	RNF146	-1.46	1.06E-03	-3.69	1.86E-04
cg22793136	PLXNC1	0.72	1.74E-03	2.03	2.79E-04
cg07062338	FGFR2	-1.12	2.48E-03	-2.00	2.46E-03
cg18941348	MCUR1	-1.06	2.53E-03	-1.62	8.73E-03
cg00232952	GAREM	-0.64	2.86E-03	-1.27	3.99E-04
cg08650290	TRIO	-1.03	2.89E-03	-3.39	3.37E-05
cg19784449	WASF2	-0.74	3.00E-03	-1.96	1.37E-03
cg10206391	ZNF577	-0.99	3.69E-03	-1.47	5.61E-03
cg18384060	PTEN	-0.89	3.76E-03	-2.41	4.23E-04
cg06164660	TMEM132C	-1.12	4.01E-03	-1.58	2.93E-03
cg04452534	MAP3K1	-0.82	4.24E-03	-1.70	7.01E-04
cg05141014	PDE4D	-1.56	4.56E-03	-4.33	1.65E-04
cg01613401	CTNNA2	-0.97	4.82E-03	-1.54	6.81E-04
cg03384318	TCF7L2	-1.32	4.83E-03	-4.46	1.62E-05
cg26428748	TPD52	-0.79	5.49E-03	-1.42	5.55E-04
cg06434738	FTO	-0.76	5.88E-03	-1.29	1.70E-03
cg17942666	BCAS3	-1.09	6.05E-03	-1.84	8.73E-03
cg14107975	MAML2	0.43	6.40E-03	1.73	1.15E-03
cg11253592	MAML2	-0.89	6.44E-03	-1.21	9.68E-03
cg15330584	CCND1	1.02	6.44E-03	2.73	9.73E-05
cg01138673	TRIO	-0.79	6.52E-03	-2.09	3.38E-05
cg03740612	CAMKMT	-0.53	6.92E-03	-1.27	9.72E-04
cg14887509	WASF2	0.64	7.31E-03	1.37	8.62E-03
cg02716173	PDLIM5	-1.25	7.44E-03	-3.94	6.47E-05
cg05316006	TCF7L2	-0.75	7.57E-03	-1.63	8.32E-04
cg03915558	OSBPL6	-1.13	7.63E-03	-2.99	7.42E-04
cg22795218	TCF7L2	-0.71	8.19E-03	-1.38	1.21E-03
cg16596493	GAREM	-1.42	8.56E-03	-2.80	4.72E-03
cg07364676	HSCB	0.72	8.59E-03	2.55	4.81E-03

cg02789362	<i>CCDC170</i>	-0.54	9.07E-03	-1.61	2.07E-04
cg23347429	<i>TMEM132C</i>	-0.59	9.39E-03	-1.64	9.30E-04
cg09933836	<i>LINC00589</i>	-0.56	9.39E-03	-1.59	9.63E-04
cg06403317	<i>TCF7L2</i>	-1.11	9.71E-03	-4.21	1.74E-05

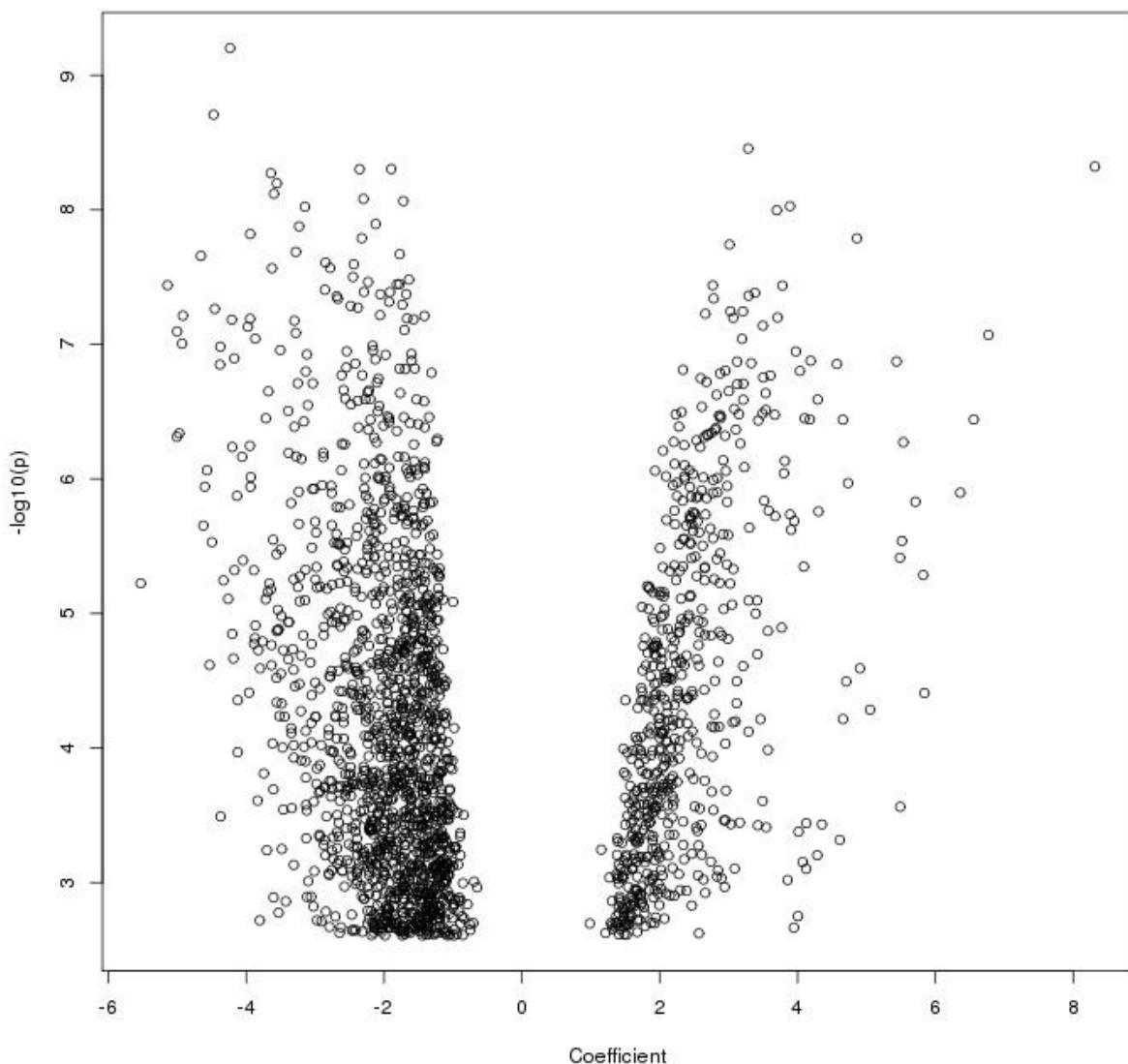
\* Abbreviations: Sister Study (SS); EPIC-Italy Study (EPIC); time to diagnosis (t2d); coefficient (coef).

## Supplementary Figures

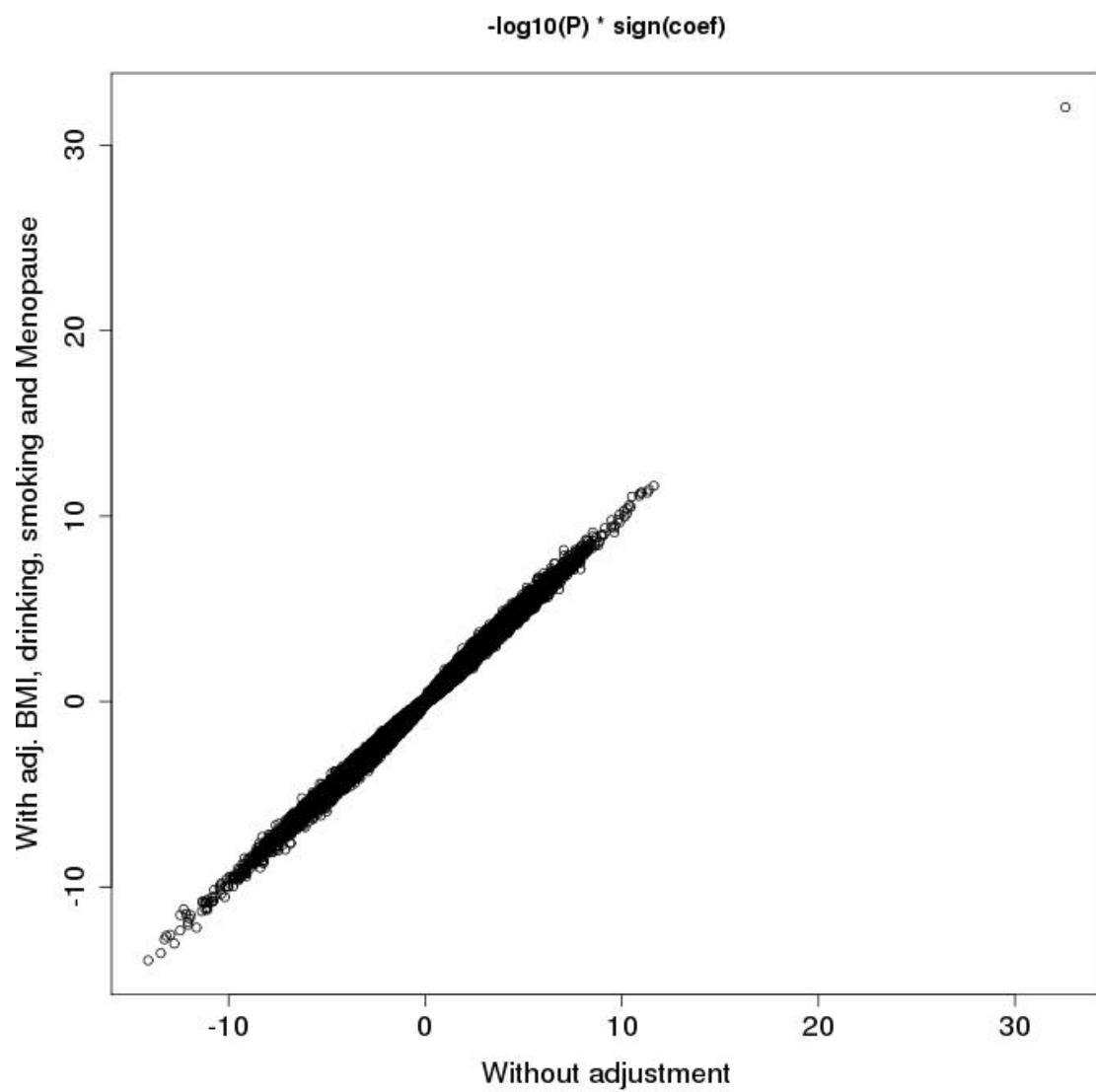
A.



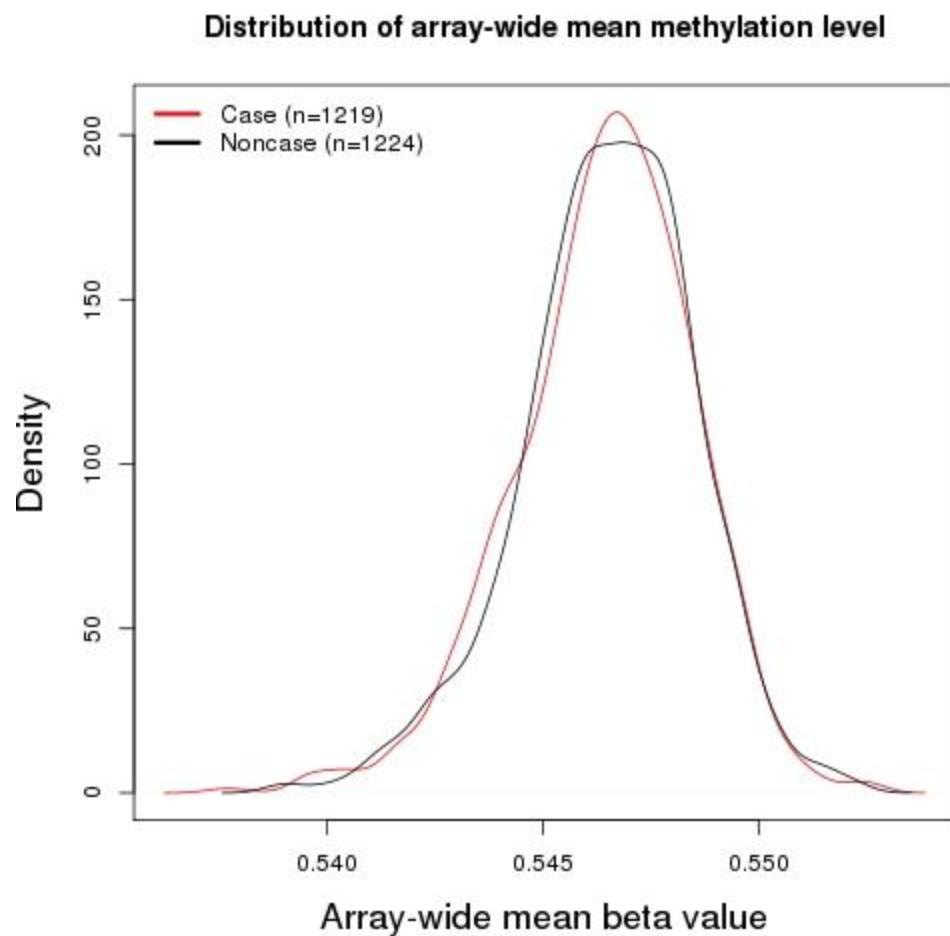
**B.**



**Supplementary Figure 1. Volcano plot for the 2,095 dmCpGs identified in Sister Study invasive breast cancer cases and replicated in EPIC-Italy dataset at FDR threshold of 0.01.**  
Shown are estimates based on (A) Sister Study data (1219 invasive cases and 1224 non-cases) and (B) EPIC-Italy data (177 controls and 152 cases).



**Supplementary Figure 2. Sensitivity analysis, comparisons of association results with or without adjusting for known breast cancer risk factors (BMI, drinking, smoking and Menopause status).** Association between each CpG and breast cancer status was tested with case cohort proportional hazard model. Shown are the comparison results of  $-\log_{10}(p) * \text{sign}(\text{coef})$  in Sister Study dataset (1219 invasive cases and 1224 non-cases).



**Supplementary Figure 3. Distribution of the average DNA methylation level across 469,412 probes on 450K array in Sister Study cases or non-cases.** Kolmogorov-Smirnov nonparametric test to check whether they are from a same distribution results in a two-sided P value of 0.47.